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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES  BE ID  AX431270  AX431270  AX431270  AX431273  AX431273  AX431273  AX431273  AX7325  AZ725  AZ7725  AZ7727	of recombinant dna-derived tpa	•	DNA linear PAT 28-JUN-2002		EU244/ CUNA Bequen 106422 Sequence 40 A14927 tPA-DNA fro	Sec	ed s	equence	equence I NA encodi	107989 Sequence 1	DNA enco	rtifici Sequence		Sequence	AR059986 Sequence R00654 CDNA encodi	A27429 cDNA sequen E01934 DNA encodin	sar Sar	equence	I01581 Sequence 1 I01583 Sequence 3	A10226 Synthetic L E01176 DNA encodit	A06611 Synthetic n	106614 Sequence 46	E01944 Synthetic	NA sequen	A27435 DNA sequenc	A27727 DNA sequenc E01945 Synthetic D	Synt	DNA	0 Sequence	Description	
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Goetz, F., Werner, R.G., Tayapiwatana, C., Manosroi, J. Methods for large scale production of recombinant dna-derived tpa or k2s molecules
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                                   CTCACCGAGTCGGGTGCCTCCTGCCTCCTGGGGAATTCCATGATCCTGATAGGCAAGGTT
                                                                                 124 TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAACATAATTACTGCCGG
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1 (bases 1 to 1068)
Niwa, M., Saito, Y., Sasaki, H., Hayashi, M., Notani, J. and Kobayashi, M.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Patent: EP 0302456-A 31 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
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I (bases 1 to 1068)

Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and

Kobayashi,M.

NovEL TISSUE PLASMINGEN ACTIVATION FACTOR

ROBAYARA PHARAGEUT CO LTD

OC Artificial genence; Genes.

PN 1989104167-A/2

PN 1988-BN 1988192320

PR 01-AUG-1988 JF 1988192320

PR 01-AUG-1987 GB 87 8718298, 26-OCT-1987 GB 87 8725052, PR

13-NOV-1987 GB 87 872683

PI NUMA MINEO, SAITO YOSHIMASA, SASAKI HITOSHI, HAYASHI MASAKO,

PI NOTANI JOJI,

PI KOBAYASHI MASAKAZU

C (212N9/64, C12N1/20, C12N5/00, C12N15/00//A61K37/54, (C12N9/64, PC

C (212N9/64, C12N1/20, C12N15/00, C12N15/00//A61K37/54, C12N15/00//CC

**SOURCE: Clone_PTTKPAdeltatrp;

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C **SOURCE: Clone_PTTKPAdeltatrp;

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C **CONTACT **C
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Synthetic DNA encoding new tissue plasminogen activator (t-PA).
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Unclassified.
1 (Dasses I to 1068)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and Niwa,M., Saito,Y., Sasaki,H., Hayashi,M.
Tissue plasminogen activator
Patent: US 5640533-A 44 24-NOV-1998;
Location/Qualifiers
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  DNA
1068 bp
44 from patent US 5840533.
                                                             AR059987.1 GI:5986437
                     Sequence
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                                                                                        CTCACCGAGTCGGGTGCCTCCTGCCTCCGTGGAATTCCATGATCCTGATAGGCAAGGTT
                                                                                                                                                     CTCACCGAGTCGGGTGCCTCCTGCCTCCGTGAATTCCATGATCCTGATAGGCAAGGTT
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                                   Indels
; Score 1065; DB 6;
; Pred. No. 4.8e-248;
0; Mismatches 0;
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Best Local Similarity 100.
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PN Artificial gequence; Genes.

PN 1989104167-A/12

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PN 1989104167-A/12

PP 01-AUG-1989 JP 1988192320

PR 01-AUG-1987 GB 87 8718298, 26-OCT-1987 GB 87 8725052, PR 13-NOV-1987 GB 87 8726681 HTOSHI, HAYASHI MASAKO, PI NUMA MINEO, SAITO YOSHIMASA, SASAKI HITOSHI, HAYASHI MASAKO, PI NOTANI JOJI,

PI NOTANI JOJI,

PI KOBAYASHI MASAKAZU

C12N9/64,C12N1/20,C12N5/00,C12N15/00//A61K37/54,(C12N9/64, PC C12N9/64,C12N1:91);

CC C12N9/64,C12N1:91);

CC ctopology: Linear;

CC topology: Linear;

CC topology: Linear;

CC *BOUTCe: Clone=pmTTK;

FH Key Location/Qualifiers

FT CDS 1. . .1170

FT CDS 1. . .1170

FT CDS 1. . .1170

FT CDS 1. . .1170
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Synthetic DNA encoding new t-PA tissue plasminogen activator.
E01945
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                                                                                                                                                                                                                                                      GGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG 1020
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C12N9/64,C12N1/20,C12N5/00,C12N15/00//A61K37/54,(C12N9/64, PC
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                                                                                                                     AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCCGAC
                                                                                                                                                                   GTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  artificial sequences.
1 (bases 1 to 1170)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and
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FUJISAWA PHARMACEUT CO LTD
OS Artificial genee
ON Artificial sequence; Genes.
PN JP 1989104167-A/12
PD 21-APR-1989
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JP 1989104167-A/12.
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1029
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Synthetic DNA encoding new t-PA tissue plasminogen activator.
E01937
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PR 03-AUG-1987 GB 87 8718298, 26-OCT-1987 GB 87 8725052, PR 13-NOV-1987 GB 87 8725683
13-NOV-1987 GB 87 8726683
PI NIWA NINEO, SAITO YOSHIMASA, SASAKI HITOSHI, HAYASHI MASAKO,
   GTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGC
                                                                                                                                                                                              781 AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
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UP 1989104167-A/4.
Synthetic construct
synthetic construct
artificial sequences.
B 1 (bases I to 1314)
S Niwa, M., Saito, Y., Sasaki, H., Hayashi, M., Notani, J. and
KODAYSHI, M.
NOVEL TISSUE PLASMINGEN ACTIVATION FACTOR
PATENT: UP 1989104167-A 4 21-APR-1989;
CS Artificial gene
OC Artificial sequence; Genes.
PN JP 1989104167-A/4
PD 21-APR-1989
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anti-sense: No;
*source: clone=pTQkPAdeltatrp;
Location/Qualifiers

    1314
/organism="synthetic construct"

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Location/Qualifiers
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strandedness: Double;
topology: Linear;
hypothetical: No;
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Niwa,M., Salto,Y., Sasaki,H., Hayashi,M., Notani,J. and
Kobayashi,M.
New tissue plasminogen activator
Patent: EP 0302456-A 35 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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1314 bp DNA linear
DNA sequence of coding region in pTQkPAdeltatrp.
A27435
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                                                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
386 c 393 g 249 t
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synthetic construct
artificial sequences.
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synthetic construct
artificial sequences.

1 (bases 1 to 1419)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and
Kobayashi,M.
New tissue plasminogen activator
Rateni: BP 0302456-A 49 08 FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Length 1419;
                                                          1021 GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065
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100.0%; Pred. No. 4.8e-248;
tive 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/hb xref="taxon:32630"
413 c 426 g 271 t
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Matches 1065; Conservative
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100.0%; Pred. No. 4.8e-248;
ive 0; Mismatches 0;
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/mol_type="genomic DNA"
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E01944 1419 bp DNA linear PAT 29-SEP-1997
Synthetic DNA encoding new t-PA tissue plasminogen activator.
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              TTTCGCATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATC
                                                                                                                                                        TTTGCCAAGCACACAGGAGGTCGCCCCGGAGAGCGGTTCCTGTGCGGGGCATACTCATCAGC
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(S Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and Kobayashi,M.

Tissue plasminogen activator

Tissue plasminogen activator

Location/Qualifiers

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62 from patent US 5840533.
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                                       GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
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Mulvihill.E.R., Nexo, B.A., Yoshitake, S., Ikeda, Y., Suzuki, S.
Hashimoto, A. and Yuzuriha, T.
Mutant t-PA with Kringle replacement
Patent: EP 0293934-A1 44 07-DEC-1988;
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llarity 100.0%; Pred. No. 4.8e-248;
Conservative 0; Mismatches 0;
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Sequence 44 from Patent EP 0293934.
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Saito, Y., Sagaki, H., Hayashi, M., Notani, J. and
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Patent: JP 1989104167-A 11 21-APR-1989;
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/organism="synthetic construct"
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ö TICCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG 600 CGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTCGGTCCGCACT 1284 120 240 480 540 099 720 AACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCAGC 60 CCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG 180 CCTCCTGCTCCACCTGCGCCTGAGACAGTACAGCCAGCCTCAG 924 GGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATC 360 HILLINGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATC 984 GGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGC 420 841 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGCGCCCCAGGCAAACTTGCACGACGCC 900 CTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACGTG GAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGCAGAATTTGAA SCTCTCTGCCTCCGTGGAATTCCATGATCCTGATAGGCAAGGTT CCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG CGGATTCGTCCCGCTGTGCCCAGGAGCAGCGTGGTCCGCACT CGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGC 0; Gaps 39)
exo,B.A., Yoshitake,S., Ikeda,Y., Suzuki,S.,
fuzuriha,T. 0%; Score 1065; DB 6; Length 1689; 0%; Pred. No. 4.8e-248; 0; Mismatches 0; Indels 0; kringle replacement 4-A1 46 07-DEC-1988; /Qualifiers 324 m≈"unknown" c 504 g B ć 8 8 8 PAT 02-DEC-1994

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Bollen,A.J., Gheysen,D., Jacobs,P., Pierard,L. and Collen,D.J.
Patent: WO 8804690-A 3 30-JUN-1988;
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Pred. No. 4.8e-248;
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                                     GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
                                                                                                             <u> GTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGC</u>
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Search completed: August 19, 2003, 04:46:36 Job time : 4472.78 secs

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August 18, 2003, 19:51:53; Search time 375.192 Seconds (without alignments) 7662.485 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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			Description	Human kringle 2 se	Sequence of coding	Sequence of coding	Sequence of coding	Sequence of coding	Novel plasminogen	Novel plasminogen	Tissue plasminogen
SUMMARIES			ΙΩ	AAD40616	AAN91120	AAN91135	AAN91123	AAN91133	AAT27588	AAT27587	AAN82178
			DB	24	10	10	70	10	17	17	6
			Match Length DB	1065	1068	1170	1314	1419	1680	1680	1689
,	*	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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(BOEH ) BOEHRINGER INGELHEIM INT GMBH.

Sequence encoding	Sequence of native	Plasmid pST112 enc	Human tPA clone.	Human tissue plasm	Sequence encoding	Plasmid pKG12 cont	Entire sequence of	Plasmid pEMp1-tPA.	Glycosylated plasm	Sequence encoding	Sequence encoding	Tissue plasminogen		Part of tPA024 gen	Part of tPA023 gen	Sequence encoding	T-PA67+ mutant wit	Human tissue plasm	Full-length tissue	Human tissue plasm	Sequence encoding	T-PA variant contg	Plasmid plgNTQTPA	T-PA with -ve char	Sequence encoding	Human tissue plasm	Plasmid plgN delta	cDNA sequence enco	cDNA of human tiss	Human tissue plasm	Human tissue type	Sequence encoding	DHFR/intron (WTras	OmpA-K2S fusion pr	Sequence encoding	
AAQ01358	AAN91119	AAQ05532	AAQ87370	AAV37294	AAN60659	AAN90542	AAN70491	AAN81970				AAN82179	AAN81090			AAQ05177	AAQ13379	ABK52546	AAT27585	AAZ31998	ø	AAQ12073	AAQ05534		AAN70248	AAQ86576	AAQ05535	AAN60146	•	ABK52545	ABL59544	AAN30001	AAT15930	AAD40614	AAQ06762	AAN91122
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1065	1065	1065	1065	1065	1065	1065	1065	1065	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1063.4	1062	1062	1061.8
6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 AAD40616

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Tissue plasminogen activator; tPA; kringle 2 serine protease; stroke; KSS; cardiaci infarction; acute mycocardial infarction; pulmonary embolism; artery occlusion; deep vein thrombosis; blood clotting; thrombolytic; cerebroprotective; cardiant; ompA; enzyme; human; gene; ds.
                                                                                                                                                                    Location/Qualifiers
1..1065
/*tag= a
/product= "Human K2S protein"
                                                                 Human kringle 2 serine protease (K2S) DNA.
 BP.
AAD40616 standard; DNA; 1065
                                                                                                                                                                                                                                                                          07-NOV-2001; 2001WO-EP12857.
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                                             (first entry)
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                                             30-OCT-2002
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                      AAD40616;
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13-NOV-1987;
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                                                                                                                                                   The present invention relates to a method of producing extracellularly secreted, active, correctly folded, recombinant tissue plasminogen activator (FPA), Kringle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants. Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vein thrombosis or related diseases associated with unwanted blood clotting. The present sequence
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                                                                    Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
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            Ä
            Manosroi
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            Manosroi J,
            Tayapiwatana C,
                                                                                                                              Claim 12; Page 31; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 1065; Conservative
            Goetz F,
                                 2002-519376/55
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                                            P-PSDB; AAE25036
                                                                                                        peptide OmpA
            Werner R,
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                                                                                                                                                       Sequence 1068 BP; 226 A; 314 C; 313 G; 215 T; 0 other;
half-life and stronger thrombolytic activity.
                                                                                      (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                            Disclosure; Page ?; 68pp; English
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coding region in plasmid pTQkPA

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                                                                                                                                                                                                                                                                                                                  (FUJI ) FUJISAWA PHARM CO LTD
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P-PSDB; AAP94409.
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Kobayashi

Notani J,

Saito Y, Sasaki H, Hayashi M,

87GB-0018298. 87GB-0025052. 87GB-0026683.

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                          Query Match 100.0%; Score 1065; DB 10; Length 1314; Best Local Similarity 100.0%; Pred. No. 1e-236; Matches 1065; Conservative 0; Mismatches 0; Indels 0;
Sequence 1314 BP; 286 A; 386 C; 393 G; 249 T; 0 other;
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                                                                                                                                                                                                                                                Sequence 1419 BP; 309 A; 413 C; 426 G; 271 T; 0 other;
                                                                                                                                 New tissue plasminogen activator - comprising finger and growth factor domains lacking longer half-life and stronger thrombolytic activity.
                                                                         Notani J,
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                                                                         Saito Y, Sasaki H, Hayashi M,
                                                                                                                                                                                     Disclosure; Page ?; 68pp; English
                                                (FUJI ) FUJISAWA PHARM CO LTD
87GB-0018298.
87GB-0025052.
87GB-0026683.
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Best Local Similarity 100.
Matches 1065; Conservative
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P-PSDB; AAP94416.
03-AUG-1987;
26-OCT-1987;
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activator (AAR96222) in which the kringle KI domain (AAR96221) of plasminogen replaces the native KI domain of tissue plasminogen activator (tPA) (AAR96220). It was obtd. by inserting a synthetic plasminogen KI domain DNA (AAT27586) into tPA cDNA and can be expressed in transformed Escherichia coli RRI cells (FERM P-9272). Novel plasminogen activators are produced that show increased clot lysing specificity or plasma half-life.
                                                                                                                                                                                                                                   ; Score 1065; DB 17; Length 1680; Pred. No. 1.1e-236; 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                   Sequence 1680 BP; 387 A; 471 C; 479 G; 343 T; 0 other;
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Matches 1065; Conservative
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                                                                                                            AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue plasminogen activator; tPA; alpha2-plasmin inhibitor; fibrinolytic; thrombolytic; fibrin; thrombosis; blood clotting; protein engineering; kringle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybrid plasminogen activator comprises human tPA activator ar
N-terminal crosslinking domain from alpha2-plasmin inhibitor
useful to treat thrombosis and image blood clots
                                                                                                                                                                                                                                                                                                                                                                                                                      GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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P-PSDB; AAR96223.
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06-JUN-1994;
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                                                                               Gaps
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                                           Score 1065; DB 17; Length
Pred. No. 1.1e-236;
                                                                               Indels
       Sequence 1680 BP; 386 A; 471 C; 480 G; 343 T; 0 other;
                                                                               ö
                                                                               0; Mismatches
                                           100.0%;
                                                                               Conservative
                                                          Similarity
                                                              Best Local Simi
Matches 1065;
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                                                                                                                                                            GCCATCATCATCAGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG
                                                          TGCCAGGCCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCATGACTTTGGTG
                                                                                                                               GCCATCATCAGCTGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTACACAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA construct (AAT27587) codes for a novel plasminogen activator (AAR96223) in which the kringle K1 domain of plasminogen (see also AAR96221) is mutated to substitute asparagine for aspartic acid at position 5, and replaces the native K1 domain of tissue plasminogen activator (tPA) (AAR96220). It was obtd. by mutagenesis of the sequence in vector Zem99-8000 (see also AAT27587). The novel protein can be expressed in Escherichia coli REI/Zem99-8010 cells (FERM P-9315). Novel plasminogen activators are produced that show increased clot lysing specificity or plasma half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue plasminogen activator; tPA; alpha2-plasmin inhibitor; fibrinolytic; thrombolytic; fibrin; thrombosis; blood clotting; protein engineering; kringle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybrid plasminogen activator comprises human tPA activator and N-terminal crosslinking domain from alpha2-plasmin inhibitor useful to treat thrombosis and image blood clots
                                                                                                                                                                                                     GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065
                                                                                                                                                                                                                        Location/Qualifiers
1..105
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel plasminogen activator DNA.
                                                                                                                                                                                                                                                                                                                                   ВР
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92US-0827587.
94US-0254485.
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106..1677
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-187699/19.
P-PSDB; AAR96222.
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06-JUN-1994;
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06-AUG-1996
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sig_peptide
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1465 AACATGCTGTGTGCTGGAGACACTCGGAGCGGGGGGGCCCCCAGGCAACTTGCACGACGCC 1524
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TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG
                                                                                                                                         TTTCGCATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCCACCCCTGGCAGGCTGCCATC
                                                                                                                                                                                                                                                                                Trreccaagcacarceccegaagcercecaagcecrerecegegegegearacrearce
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                                    AATCCTGATGGGGATGCCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG
                                                                     AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG
                                                                                                      TITGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGGCATACTCATCAGC
                                                                                                                                                                                                                                                                                                                     TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGAGTTTCCGCCCCACCACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified tissue plasminogen activator - having glycine-183 and serine-186 residues sustd. with serine and threonine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One N-glycosylation site, i.e. NSS (117-119) is substituted with NSM and the N-glycosylation is removed.

Plasmid encoding the modified tPA is 99-6300 and its transformant is E.coli RR1.-Zem 99-6300 (FERM P-9127).

This modified tPA, used to treat thrombosis, is of high quality and has a longer half life period in blood.

See also AAN82177-N82179.

(Updated on 10-MAR-2003 to add missing OS field.)

(Updated on 25-WAR-2003 to correct PF field.)

(Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; tPA; thrombosis; N-glycosylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1689;
                    1065
                                    1636 GTTACCAACTACCTAGATTGGTGACAACAACATGCGACCGTGA 1680
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                  GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA
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                                                                                                                                                                                                                                                                                Tissue plasminogen activator with S-119 substd for M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1065; DB 9;
Pred. No. 1.1e-236;
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                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..1689
/*tag= a
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Matches 1065, Conservative
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P-PSDB; AAP82581.
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                                                                                                          TTTGCCAAGCACACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGGCATACTCATCGC
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           Wild type tissue plasminogen activator (t-PA); infarction treatment; thrombosis treatment; embolism treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tissue plasminogen activator (t-PA) analogue -
with higher fibrin selectivity than native t-pa, useful for
treating infarction, thrombosis and embolism
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/note="synthetic 3' adaptor"
                                                                                                                                       adaptor'
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                                                                                                                                    /note="synthetic 5'
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                                                                                        Location/Qualifiers
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Matches 1065; Conservative
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                                                      1189 GTCGAAAAATACATTGTCCATAAGGAATTCGATGACACTTACGACAATGACATTGCG
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                           541 GTCGAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
                                                                                                                      CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequence of native tPA gene is excised from plasmid pST112, digested with Bamili and SalI to form plasmid pST118. (Updated on 03-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tissue plasminogen activator - comprising finger and growth factor domains lacking tPA for longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1065; DB 10; Length Best Local Similarity 100.0%; Pred. No. 1.1e-236; Matches 1065; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2100 BP; 498 A; 595 C; 597 G; 410 T; 0 other;
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Location/Qualifiers
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                   (FUJI ) FUJISAWA PHARM CO LTD
                                                                                                                                                                                                                                       87GB-0018298.
87GB-0025052.
87GB-0026683.
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P-PSDB; AAP94406.
                                                                                                                                                                                                                                                              26-OCT-1987;
13-NOV-1987;
                                                                                                                                                                                           02-AUG-1988;
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                      1429 AGACTGTACCCATCCAGCCGCTGCACATCACAACATTACTTAACAGAACAGTCACCGAC
                                                        AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGCCCCCAGGCAAACTTGCCACGACGCC
                                                                                 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGCCCCAGGCAAACTTGCACGACGCC
                                                                                                             TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTGTAACGATGGCCGCATGACTTTGGTG
                                                                                                                                                                GGCATCATCAGCTGGGGCCTGTGGACAGAAGGATGTCCCCGGGTGTGTACACAAAG
     AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                      Intron, recombination, combinatorial gene, trans-splicing, gene therapy, polymerase chain reaction, PCR; primer; amplification, tissue plasminogen activator, tPA; plasmid TPA-KS+; thrombolytic;
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/note= "signal sequence and finger-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New intron-mediated recombinant techniques - used for the generation and selection of novel genes and gene prods. for use in therapy
                                                                                                                                                                                                                    GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065
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/product= Kringle-2 domain
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/product= EGF-like domain
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                                                                                                                                                                                                                                                                                                                                                                                                             Human tPA clone.
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                                                                                                                                                                                                                                                           Gaps
                                                                                                                   tPA with N-terminal peptide of plasminogen linked is more stable in vivo than the native form. It is useful as a thrombolytic agent in the treatment of vascular diseases eg myocardial infarction,
                                     tissue plasminogen activator - having N-terminal peptide of sminogen linked to tissue plasminogen activator for increased
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                                                                                                                                                                                                                               Query Match
100.0%; Score 1065; DB 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-236;
Matches 1065; Conservative 0; Mismatches 0;
                                                                                                                                                                           PA field.)
                                                                                                                                                                         (Updated on 25-MAR-2003 to correct
                                                                                           Disclosure; Page ?; ?pp; English.
                                                                                                                                                              pulmonary embolism etc.
WPI; 1990-232757/31.
P-PSDB; AAR06237.
                                                  plasminogen linked stability in vivo.
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                                                                                                             GGCATCATCAGCTGGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACAAAG
                                                                                                                                                                                                                  GGCATCATCAGCTGGGGCCTGTGGACAGAAGGATGTCCCCGGGTGTACACAAAG
AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGCCCCCAGGCAAACTTGCACGACGCC
                                                                                    TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTGTGAACGATGGCCGCATGACTTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reverse splicing construct containing fragments of autocatalytic introns - able to cleave and ligate discontinuous nucleic acid for generating new genes and e.g. ribozymes, libraries of enzymes and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , bond;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "signal sequence and finger-like domain"
335..447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pINVI; reverse-splicing intron; group II intron;
exon binding site; domain V motif; branch site acceptor;
nucleophilic group; transesterification; phosphodiester bond
autocatalytic Y-branched intron; reverse splicing reaction;
                                                                                                                                                                                                                                                                                     GTTACCAACTACCTAGACTGGATTCGTGAACATGCGACCGTGA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tissue plasminogen activator gene sequence.
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/note= "Kringle-1 domain
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/note= "catalytic domain"
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/note= "EGF-like domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/note= "Kringle-2
973..2162
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                                                                                                                                                                                                                                                                                                                             Gaps
                                     A cDNA clone of human tissue plasminogen activator (tPA) was amplified by PCR using the primers given in AA087368-69. The amplified tPA DNA (AA087370) was ligated into vector KS+ to obtain plasmid TPA-KS+. The construct was used in combinatorial methods involving RNA splicing-mediated shuffling of tPA domains improved thrombolytic properties.

(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                      Sequence 2162 BP; 520 A; 606 C; 619 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                            ; Score 1065; DB 16;
; Pred. No. 1.1e-236;
0; Mismatches 0; 1
    4; Page 59-60; 87pp; English
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                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 1065; Conservative
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The present sequence represents the human tissue plasminogen activator gene. It was used to construct plamsid TPA-KS+, which is used in the course of the invention. The specification describes a purified reverse oblicing intron which comprises a segment comprising a reverse-splicing intron which comprises a segment comprising a sequent of a group II intron, including an exon binding site not naturally present in the intron and a second segment comprising a parent of a group II intron, including a domain V motif, a branch site acceptor, and a nucleophilic group for transesterifying a phosphodiester bond of an RNA. Together the two segments form an a ucocatalytic Y-branched intron which catalyses integration of at least the first segment into substrate RNA by a reverse splicing reaction. The reverse-splicing introns are used, by specific cleavage and ligation of discontinuous nucleic acid, to generate new genes and gene products, e.g. ribozymes (for use in gene therapy or as reagents in DNA manipulation, e.g. replacements for restriction enzymes) or immunologically active or signal-transducing proteins such as antibody
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                                                                                                                                                                                                                                                                    Sequence 2162 BP; 520 A; 606 C; 619 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 1065; Conservative
                                                                                                                                                                                                                                          and enzyme libraries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence encoding human pre-tissue plasminogen activator (pre-t-PA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant forms of human tissue plasminogen activator- having higher specific activity and resistance to conversion to two chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patentors claim a novel recombinant human t-PA which is resistant to specific enzymatic cleavage because it is stabilised site-directed mutagenesis at a 2-chain cleavage site. Partic. the natural Arg at position 275 is replaced by Gly or Glu, or Ile at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen conversion; vascular disease therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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01-APR-1986;
22-APR-1985;
01-APR-1986;
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22-JUL-1991
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(Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1065; DB 10; Length 2560; 100.0%; Pred. No. 1.1e-236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            t-PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tissue plasminogen-activator gene; pKG12;
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                                                                                                                                                                                                                                                                                                                     standard; cDNA;
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                                                                                                                                                                                                                                Gaps
position 276 is replaced (275 and 276 refer to the posn. of the AAs in the mature protein; i.e. AAs 310 and 311 of AAP60790). Also new [1] DNA sequences; (2) expression vectors; and (3) microorganisms and cell cultures transformed with these vectors. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                             ö
                                                                                                                                                                                    Length 2547;
                                                                                                                                                                                                                             Indels
                                                                                                                                        Sequence 2547 BP; 627 A; 688 C; 691 G; 541 T; 0 other;
                                                                                                                                                                                  5; DB 7;
1.1e-236;
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                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                  Score 1065;
Pred. No. 1.
                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                      Best Local Similarity 100.
Matches 1065; Conservative
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	TGCCGG        TGCCGG	ACGTGG        ACGTGG	CCTCAG 	GCCATC 	ATCAGC        ATCAGC	CACCTG          CACCTG	TTTGAA        TTTGAA	ATTGCG	CGCACT        CGCACT	700000 	CATGTC	ACCGAC        ACCGAC	SACGCC        SACGCC	TTGGTG	ACAAAG	ACAAAG		
	FAATTAC         FAATTAC	PAGGCTG	PAGCCAG	SCAGGCT 	ATACTC	CCCCAC	CAGAAA         CAGAAA	PATGAC	STGGTC	GAGCTC	GAGGCT        GAGGCT	ACAGTC        ACAGTC	TTGCAC	ATGACT	GTGTAC	Grerac	065	٠
GATCCT	CAAACA:         CAAACA:	GAACCG(        GAACCG(	ACAGTAC        ACAGTAC	00000000000000000000000000000000000000	)         -	GTTTCC         GTTTCCC	GGAGGAC         GGAGGAC	TTACGAC         TTACGAC	GAGCAGO	GGAGTG1 	GCTGAAC         GCTGAAC	TAACAGI         TAACAGI	GCCAAAC         GCCAAAC	reeccec         reeccec	CCCGGG3	CCCGGG		
	SCTGGG         SCCTGGG	GCTGAA 	SCCTGAG	CTCCCA 	CCTGTG         CCTGTG	AGGAGAG        AGGAGAG	TGGCGA	TGACAC        TGACAC	CCAGGA        CCAGGA	CTGGAC	GGAGCG	TTTACT	GCCCCA 	GAACGA	GGATGT	GGATGT	GCGACO	
CGTGGA	CACTGG 	GCCACG 	CCTGCG 	ACATCGC         ACATCGC	AGCGGTT         AGCGGTT	GCTTCC/ 	TGGTCC         TGGTCC	TCGATGA         TCGATGA	GCTGTGC         GCTGTGC	TGCCGG/ 	TCTATTO        TCTATTO	CACAAC!          CACAAC!	30333333333333333333333333333333333333	rererci         rererci	GACAGAZ	gacagaz	ACAACA1	
	TACACAGGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG 	AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGGCAGGCTGAACCGCAGGCTGCAGGCTGCTGGATGCCAGGCCCTGGTGCCACGTGCTGCTGATGGGAGAACCGCAGGCTGACGTGCAAGCCCTGGTGCCACGTGCTGATGAAACAAGCAGGCTGACGTGCAAGCAA	GAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGC	TITCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGTGCCATC 	TTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGGATACTCATCAGC 	TCCTGCTGGATTCTCTCTGCGCCCCACTGCTTCCAGGAGGAGGTTTCCGCCCCACCTG	CGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGGAGCAGAATTTGAA 	GTCGAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG 	CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACT 	GIGIGCCTICCCCGGGGGCCTGCAGCTGCGGACTGGAGGGAGTGTGAGCTCTCCGGC 	TACGGCAAGCATGAGGCCTTGTCTCTTTCGAGGGGGGCGGCTGAAGGAGGCTCATGTC	agactgtacccatccagccgctgcacatcacaacatttacttaacagaacagtcaccgac 	AACATGCTGTGCTGGAGACACTCGGAGCGGGGGGGGGCCCCAGGCAACTTGCACGACCCCAGACATTGCACGAACGCCCAGGCAAGCTTGCACACGCCCAGGCAAGCTTGCACACGCCCAGGCAAGCTTGCACACGCCCAGGCAAGCAAACCAAGCAAACCAAGCAAACCAAGCAAACCAAGCAAACCAAGCAAACCAAGCAAACCAAGCAAGCAAACAAACAAACAAACAAACAAACAAACAAAA	TGCCAGGCGATTCGGGAGGCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG 	GGCATCATCAGCTGGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG	secrere	GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 	
GCCTCC	CCCAGTC 	GCCAAGG	CCCTCC 	6660TC 	AGGTCGC         AGGTCGC	101600 	AGAACAT          AGAACAT	GTCCATA         GTCCATA	TCGGATT         TCGGATT	GCGGACC         GCGGACC	6007761 	AGCCGCT          AGCCGCT	GGAGAC?          GGAGAC?	GGAGGCC          GGAGGCC	96CCTG	GCCTG	GACTGGP         GACTGGP	
TCGGGT	CAGAAC         CAGAAC	GGGGAT        GGGGAT	CATGTG         CATGTG	PAAAGGA        PAAAGGA	CACAGG	ATTCTC         ATTCTC	777666C         777666C	TACATT	CTGAAA 	900000 	CATGAG	CCATCC	TGTGCT	GATTCG         GATTCG	AGCTGG	AGCTGG	TACCTA	
CACCGAC	CACAGC	TCCTGA1         TCCTGA1	GTACTG         GTACTG	TCGCATC         TCGCATC	TGCCAAC         rGCCAAC	CTGCTGC	GGTGATC	CGAAAA         CGAAAA	SCTGCAC         SCTGCAC	316CC11         316CC11	GGCAAG          GGCAAG	ACTGTAC          ACTGTAC	CATGCTC	ccaeeec	CATCATO	carcard	TACCAAC         TACCAAC	
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Search completed: August 18, 2003, 23:28:54 Job time : 376.192 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

August 18, 2003, 22:51:23 ; Search time 83.3499 Seconds (without alignments) 5639.757 Million cell updates/sec Run on:

US-09-987-455-7 1065

Perfect score:

1 tctgagggaaacagtgactg......gtgacaacatgcgaccgtga 1065 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

569978 segs, 220691566 residues Searched:

Total number of hits satisfying chosen parameters:

1139956

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:\* Database :

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/cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
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/cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	1065	100.0	1068	~	US-08-811-949-44	Sequence 44, Appl
7	1065	100.0	1419	N	US-08-811-949-62	62,
m	1065	100.0	1848	ო	US-08-814-412-10	10,
4	1065	100.0	2101	N	US-08-811-949-42	42,
S	1065	100.0	2162	ч	US-08-119-512-3	3, 1
9	1065	100.0	2162	٦	US-08-488-015B-3	Sequence 3, Appli
7	1065	100.0	2162	Н	US-08-488-015B-25	25,
æ	1063.4	99.8	1170	~	US-08-811-949-64	64
σ	1063.4	99.8	1314	7	US-08-811-949-48	48,
10	1063.4	99.8	1738	9	5200340-1	. 520
11	1063.4	99.8	1955	7	US-08-883-795A-39	ന
12	1063.4	99.8	2457	9	5344773-1	53.
13	1063.4	99.8	7360	Н	US-08-286-740-1	Sequence 1, Appli
14	1063.4	99.8	7360	Ŋ	PCT-US95-09576-1	<u>۔</u>
15	1061.8	99.7	1068	7	US-08-811-949-46	46
16	1061.8	99.7	1314	~	US-08-811-949-50	50,
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18	1057	99.5	1068	7	US-08-811-949-52	52
19	1057	99.5	1314	7	US-08-811-949-54	54
20	1056.4	99.5	1068	Н	US-08-137-116-2	7
21	1056.2	99.5	1137	4	US-09-553-498-9	Sequence 9, Appli
22	1056.2	99.5	1137	4	US-09-618-869-9	6
23	1055.4	99.1	1170	~	US-08-811-949-66	99
24	1054.8	99.0	1065	-	US-08-427-640-1	Sequence 1, Appli
25	1053.8	98.9	1314	7	US-08-811-949-56	26
26	1050	98.6	1068	9	5223256-3	Patent No. 5223256
27	1046.8	98.3	1065	~	US-08-427-640-5	Sequence 5, Appli

100.0%; Score 1065; DB 2; Length 1068;

Query Match

Sequence 58, Appl Sequence 3, Appli Sequence 60, Appl Patent No. 5185259 Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 40, Appli Sequence 40, Appli Patent No. 5244676 Sequence 7, Appli Sequence 7, Appli Sequence 122, Appli Sequence 122, Appli	Sequence 122, App Sequence 122, App Patent No. 5188829
US-08-811-949-58 US-08-427-640-3 US-08-811-949-60 5185259-2 US-08-427-640-7 US-08-410-882-5 5244676-4 US-08-811-949-40 5200340-3 5200340-3 US-08-811-949-40 US-08-811-949-40 US-08-811-949-40 US-08-811-949-40 US-08-811-949-40	US-09-542-615A-122 US-09-606-421B-122 5188829-2
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1041 1035.4 1035.4 1033.9 92.4 92.4 801.6 626.6 625.7 472 472 472 170.8	170.8 170.8 170.8
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## ALIGNMENTS

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Sequence 44, Application US/08811949
; Sequence 44, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SAJTO, YOSHIMASA
APPLICANT: SAGAKI, HITOSHI
APPLICANT: HAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: DELON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
APPLICANT: ALLINGTON
CITY: ARLINGTON
CITY: ARLINGTON
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FLING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-413-3000
TELEFAX: 703-413-220
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION:
US-08-811-949-44
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TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG
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                                                                                                                                            APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: HAYASH, HITOSHI
APPLICANT: HAYASH, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1419;
            1024 GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: OS-MAR-1997
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELEPHONICATION INFORMATION:
TELEPHONICE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1065; DB 2;
llarity 100.0%; Pred. No. 1.5e-291;
Conservative 0; Mismatches 0;
                                                                                               ; Sequence 62, Application US/08811949
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MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
Matches 1065; Conserv
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; LOCATION:
US-08-811-949-62
                                                                               US-08-811-949-62
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                                                                                               GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
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                              Indels
              Pred. No. 1.4e-291;
Mismatches 0;
100.08;
                            Matches 1065; Conservative
              Best Local Similarity
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594

180

120

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414

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Gaps

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,412
FILING DATE: 11-MAR-1997
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jarrell Ph.D., Brenda H.
REGISTROCE/DOCKET NUMBER: 39,223
REFERENCE/COCKET NUMBER: 0079571-0040
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 617 248 5000
INFORMATION FOR SEQ ID NO:
SEQUENCE CRARACTERISTICS:
LENGTH: 1848 base pairs
                                                                                                                                                                                                                                                                                                                                                           ; CLONE: amplified t-PA clone US-08-814-412-10
                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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IMMEDIATE SOURCE:
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                    655 TTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGCAGGCTGCCATC
                                                                                                                TTTGCCAAGCACACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGC
                                                                                                                                             TTTGCCAAGCACAGGAGGTCGCCCGGAGGCGGTTCCTGTGCGGGGGCATACTCATCAGC
                                                                                                                                                                              TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGGAGGTTTCCGCCCCCACCACCTG
                                                                                                                                                                                                                                            ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAA
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US-08-814-412-10
; Sequence 10, Application US/08814412
; Patent No. 6150141
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    Length 1848;
                                              Indels
  100.0%; Score 1065; DB 3;
100.0%; Pred. No. 1.7e-291;
tive 0; Mismatches 0;
Query Match
Best Local Similarity 100.0
Matches 1065; Conservative
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APPLICANT: Jarrell Ph.D., Kevin A.
TITLE OF INVENTION: Intron-Mediated Techniques and Reagents
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate, Hall & Stewart

STREET: 53 State Street CITY: Boston STATE: MA COUNTRY: USA

ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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Query Match
Best Local Similarity 100.0
Matches 1065; Conservative
                      CDS
25..1710
                      NAME/KEY:
                                          ; LOCATION:
US-08-811-949-42
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
COUNTRY: VA
COUNTRY: USA
ZIP: 22202
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MEDIUM TYPE: Floppy disk
COMPUTER: END FO Compatible
COMPUTER: Floppy disk
COMPUTER: F
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APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 677
CORRESPONDENCE ADDRESS:
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Patent No. 5840533
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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Length 2101;
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  DB 2;
                  Pred. No. 1.8e-291;
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                                        0; Mismatches
    Score 1065;
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1186 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGGAGAAATTTGAA 1245
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                                                                                                                                                                 766 CTCACCGAGTCGGGTGCCTCCTGCCTCCGTGAATTCCATGATCCTGATAGGCAAGGTT
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                                                                                                                                                                                                                                                    826 TACACAGCACAGAACCCCAGTGCCCCAGGCACTGGGCCTGGGCCAAACTAATTACTGCCGG
                                                                                                                                                                                                                                                                                                                181 AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG
                                                                                                                                                                                                                                                                                                                                              886 AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGTGGTGGG
                                                                                            61 CTCACCGAGTCGGGTGCCTCCTCCCCTCGAATTCCATGATCCTGATAGGCAAGGTT
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      Indels
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      Mismatches
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      Matches 1065; Conservative
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1609 GGCATCACCACGCTGGGCCTGGGCCTGTGGAAGGATGTCCCGGGTGTGTACACAAAG
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                                                                                                                                                                                                               US-08-119-512-3
; Sequence 3, Application US/08119512
; Sequence No. 5498531
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
                                                                                       GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065
                                                                                                            1669 GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1713
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LOCATION: 82..334
OTHER INFORMATION: /product= "Signal Sequence and
OTHER INFORMATION: Finger-like domain"
FEATURE:
NAME/KEY: misc feature
LOCATION: 335..447 /product= "EGF-like domain"
FEATURE:
FEATURE:
FEATURE:
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LOCATION: 448.714
OTHER INFORMATION: /product= "Kringle-1 domain"
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LOCATION: 715..972
OTHER INFORMATION: /product= "Kringle-2 domain"
FEATURE:
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LOCATION: 973..2162

COTHER INFORMATION: /product= "Catalytic domain"

// OTHER INFORMATION: /product= "Catalytic domain"
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TROPPY disk
COMPUTER: TROPPY disk
COMPUTER: TROPS FLODS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,512
FILING DATE: 10-SEP-1993
CLASSIPICATION: 435
ATTORNEST PROTENT HORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HUI-008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELECAMONICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
ENGINE ALCOMMUNICATION SEQ ID NO: 3:
LENGTH 2162 base paire
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: other nucleic acid
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Best Local Similarity
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NAME/KEY:
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                                                                                                  Kevin A.
INTRON-MEDIATED RECOMBINANT TECHNIQUES
AND REAGENTS
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LOCATION: 82.334
OTHER INFORMATION: /product= "Signal Sequence and
Patent No. 5780272
OTHER INFORMATION: Finger-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/REY: misc_feature
LOCATION: 715..972
OTHER INFORMATION: /product= "Kringle-2 domain"
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LOCATION: 973.7162
OTHER INFORMATION: /product= "Catalytic domain"
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                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PEPLICATION NUMBER: US/08/488,015B
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: VINCent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 140,008.02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 832-1000
                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: other nucleic acid
                                                 Sequence 3, Application US/08488015B
Patent No. 5780272
GENERAL INFORMATION:
                                                                                                                                                                                          ADDRESSEE: Foley, Hoag & Bliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 335.7447
OTHER INFORMATION: /product=
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LOCATION: 448.714
OTHER INFORMATION: /product=
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Matches 1065, Conservative
                                                                                                 APPLICANT: Jarrell, Kev
TITLE OF INVENTION: INTI
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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STREET: CLLL
TTV: BOSTON
                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                           CITY: Bosto
STATE: MA
COUNTRY: US
ZIP: 02109
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CTCACCGAGTCGGGTGCCTCCTGCCTCCTGTGTTTCCATGATCCTGATAGGCAAGGTT
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CTCACCGAGTCGGGTGCCTCCTGCCTCCGTGGAATTCCATGATCCTGATAGGCAAGGTT 120

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US-08-488-015B-25; Sequence 25, Application US/08488015B 2 Patent No. 5780272; Patent INFORMATION:

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            1186 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGGAGAAATTTGAA 1245
                                                                       1246 GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACATTACGACAATGACATTGCG 1305
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASATI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
WINMARE OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
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FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 64, Application US/08811949; Patent No. 5840533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Jarrell, Kevin A.
TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
TITLE OF INVENTION: AND REAGENTS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION DATE:
APPLICATION DATE: US/08/488,015B
FILING DATE: 07-JUN-1995
ATTORNEY, AGENT INPORMATION:
NAME: VINCENC, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELECOMUNICATION INPORMATION:
TELECOMUNICATION INPORMATION:
TELECOMUNICATION INPORMATION:
                                                                                                   ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 832-70100
INFORMATION FOR SEQ ID NO: 25.
SEQUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-488-015B-25
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                                                                                                                                          CITY: BOS
STATE: MA
COUNTRY:
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Matches 1065;
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886 AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC 945
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                                        941 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGCCCCAGGCAAACTTGCACGACGCC
                                                                                                                        901 TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                           US-08-811-949-48

Sequence 48, Application US/08811949

Sequence 48, Application US/08811949

Patent No. 5840533

GENERAL INFORMATION:
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HOTANI, JOUJI
APPLICANT: HOTANI, JOUJI
APPLICANT: NORAYASHI, MASAKAZU
ITILE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY, ARLINGTON
                                                                                                                                                                                                                                                                                    GTTACCAACTACATGGATTCGTGACAACATGCGACCGTGA 1065
                                                                                                                                                                                                                                                                                                                          Griaccaactacciagaciggaricergacaacargcgaccgrga 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-90
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 99.9%;
Matches 1064; Conservative (
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TELEFAX: 703-413-2220
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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              TELEPHONE: 703-413-3000
TELEPRAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 64: SEQUENCE CHARACTERISTICS:
LENGTH: 1170 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.9
Matches 1064; Conservative
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; NAME/KEY:
; LOCATION:
US-08-811-949-64
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
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                                                SEQUENCES:
                                                                                                                 Similarity
           5200340
                                                                                     LENGTH: 1738
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Best Local Simi
Matches 1064;
                                               NUMBER OF
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   5200340-1; Patent No.
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                                                              AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG
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1059 1179 ö 1119 1239 1299 1359 AGACTGTACCCATCCAGCCGCTGCACACACACATTACTTAACAGAACAGTCACCGAC 1479 840 669 120 759 180 819 240 879 300 939 360 666 420 480 540 900 99 720 780 9 880 GAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGCGCCTGAGACAGTACAGCCCACCTCAG 1000 TTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGCGCGCGTACTCATCATCAGC GTGTGTCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCCGGC GCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCACAGC CTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTT CTCACCGAGTCGGGTGCCTCCTGCTCCCGTGGAATTCCATGATCCTGATAGGCAAGTT TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG 760 TACACAGCACAGAACCCCCAGTGCCCAGGCCTGGGCCTGGGCAAACATAATTACTGCCGG AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG TTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGGATACTCATCAGC TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGGTTTCCGCCCCACCAC TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGGTTTCCGCCCCACCTG GTCGAAAAATACATTGTCCATAAGGAATTCGATGACACTTACGACAATGACATTGCG GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGCG TTTCGCATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCCACCCCTGGCAGGCTGCCATC ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAA CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGGAGCGCGTGGTCCCCT GTGTGCCTTCCCCCGGCGGACCTGCACGGCACTGGACGGAGTGTGAGGCTCTCCCGGC AGACTGTACCCATCCAGCCGCTGCACATCACATTTACTTAACAGAACAGTCACCGAC Score 1063.4; DB 6; Length 1738; Pred. No. 4.8e-291; 0; Mismatches 1; Indels 0; APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA, PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUB PLASMINOGEN; ACTIVATORS 1420 781 ద ò

Oy 121 TACACAGCACAGAACCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG 180	TTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCCCCCCC			Qy         901 TGCCAGGGGATTCGGGAGGCCCCTGGTGTCTGAACGATGGCGGCATGACTTTGGTG         960           lb1	RESULT 12 5344773-1 ;Patent No. 5344773 APPLICANT: WEI, CHA-MER;HSIUNG, NANCY;REDDY, VERMURI B.; ;LEMONTT, JEFFREX F.;DACKOWSKI, WILLIAM;DOUGLAS, RICHARD; ;COLE, EDWARD S.;PURCELL JR., RICHARD D.;LAU, DAVID TAI-YUI ; TITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINGGEN
00   00   00   00   00   00   00   0	Oy 1021 GTTACCAACTACCTAGATTCGTGACAACATGCGACCGTGA 1065	APPLICANT: Awang, Gregor TITLE OF INVENTION: Recombinant DNA Molecules and Expression TITLE OF INVENTION: Recombinant DNA Molecules and Expression TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: BERESKIN & PARR STREET: 40 King Street West CITY: Toronto STRIE: Ontario COUNTRY: Canada ZIP: MSH 3Y2 COMPUTER READABLE FORM:	### MEDIUM TYPE: Floppy disk  COMPUTER: IEM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.25  CURRENT APPLICATION DATA:  FILING DATE: 27-UN-1997  CLASSIFICATION: 435  ATTORNEY/AGENT INFORMATION:  NAME: Gravelle, Micheline  REGISTRATION NUMBER: 740,261  REFERENCE/DOCKET NUMBER: 740,261  TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION SEQ. 1311  TELECAM: (416) 361-1398  INFORMATION FOR SEQ. ID NO: 39:	; SEQUENCE CHARACTERISTICS: ; LENGTH: 1955 base pairs ; TYPE: nucleic acid ; ORIGINAL SOURCE: ; ORANISM: Homo sapiens ; ORANISM: Homo sapiens US-08-083-795A-39  Query Match 99.8%; Score 1063.4; DB 2; Length 1955; Best Local Similarity 99.9%; Pred. No. 5e-291; Matches 1064; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	TGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGC   TGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGC   TGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGC   TGAGGGGTCACCTGCCTCCGTGGAATTCCATGATCCTGATAGGCACTGATAGGCACTGATAGGCACTGATAGGCACTGATAGGCACGAGAATTCCATGATAGGCACTGATAGGCACGAGGCACGAGGCACGAGGCACCCGTGGAATTCCATGATCCTGATAGGCACTCCCGTGGAATTCCATGATCCTGATAGGGCACACCGAGGAATTCCATGATCCTGATAGGCACGAGCACGAGGAATTCCATGATCCTGATAGGGCACGCCACGAGGCATAGGCACGAGGCATAGGCACGAGGAATTCCATGATAGGGCACGCAC

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1657
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                                                                                                                                                                                                               1021 GTTACCAACTACCTAGACTGGATTCGTGACCAACATGCGACCGTGA 1065
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                 KESULT 13
US-08-286-740-1
Sequence 1, Application US/08286740
Fatent No. 5561053
GENERAL INFORMATION:
APPLICANT: Crowley, Craig W.
TITLE OF INVENTION: METHOD FOR SELECTITLE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 79
REFERENCE/DOCKET UNBER: 79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY-AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7360 bacc
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Matches 1064; Conservative
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STRANDEDNESS: double
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US-08-286-740-1
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                                                                                                                                                                                                                              Score 1063.4; DB 6; Length 2457;
Pred. No. 5.5e-291;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                        TCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCG
; ACTIVATOR PRODUCED BY RECOMBIANT DNA
; CURRENT OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/782,686
; FILING DATE: 01-0CT-1985
; APPLICATION DATE:
; APPLICATION NUMBER: 656,770
; FILING DATE: 01-0CT-1984
                                                                                                                                                                                                                         99.8%;
                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.9
Matches 1064; Conservative
                                                                                                                                                   SEQ ID NO:1:
; LENGTH: 2457
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ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09576
FILING DATE:
CLASSIFICATION DATE:
APPLICATION DATE:
RIGHT APPLICATION DATE:
APPLICATION DATE:
TLING DATE:
CLASSIFICATION DATE:
APPLICATION PROPRIET OF AUG-1994
ATTORNEY AGENT INFORMATION:
            STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/22-1994
TELERX: 415/952-9881
TELEX: 910/311-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           NAME: Lee, Wendy M.
REGISTRATION NUMBER: OC
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                             7360 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-09576-1
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Score 1063.4; DB 5;
Pred. No. 8.7e-291;
0; Mismatches 1;
      Query Match
Best Local Similarity 99.9%;
Matches 1064; Conservative (
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RESULT 14
PCT-US95-09576-1
Sequence 1, Application PC/TUS9509576
GENERAL INPORMATION:
APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
TITLE OF INVENTION: HOST CELLS
INUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:

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                                                                                                                                                                                                                                Score 1061.8; DB 2; Length 1068; Pred. No. 1.1e-290; 0; Mismatches 2; Indels 0;
                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                      99.7%;
                                                                   1068 base pairs
703-413-3000
        TELEFAX: 703-413-220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pair
                                                                                                                                                                                                                                                                       Conservative
                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
Matches 1063; Conserv
                                                                                                                                                                    CDS
TELEPHONE:
                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                      ; LOCATION:
US-08-811-949-46
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                              GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
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          GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
                                                                            CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGAGCAGCGTGGTCCGCACT
                                                                                               CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGCACGTGGTCCGCACT
                                                                                                                                             GTGTGCCTTCCCCCGGCGGACCTGCAGCTGCGGACTGGACGGAGGTGTGAGCTCTCCGGC
                                                                                                                                                                 GTGTGCCTTCCCCCGGCGGACCTGCCGGACTGGACGGAGTGGAGCTCTCCGGC
                                                                                                                                                                                                                 TACGGCAAGCATGAGGCCTTGTCTCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPOTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
COMPOTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: 05-MAR.1997
FLING DATE: 05-MAR.1997
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAMM: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SIAITO, YOSHIMASA
APPLICANT: SASATO, YOSHIMASA
APPLICANT: SASAH, INFO
APPLICANT: HAYASHI, MASAKO
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
ITILE OF INVENTION: TISSUE FLASMINOGEN ACTIVATOR
CORRESPONDENCES: 67
CORRESPONDENCES: 67
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUS
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.C. STREETS ALINGTON SUITE SITATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 46, Application US/08811949 ; Patent No. 5840533
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US-08-811-949-46
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841 AACATGCTGTGTGTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCC 900	AACATGCTGTGTGCTGGGGGCACCTCGGAGCGGCCCCCAGGCAAACTTGCACGACGCC 903	TGCCAGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCATGACTTTGGTG 960	TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG 963	GGCATCATCACTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG 1020	GGCATCATCAGCTGGGGCCTGGGCTGTGTGTTTTTTTTTT	1021 GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065		Search completed: August 19, 2003, 08:35:12 Job time : 85.3499 secs
841	844	106	904	961	964	1021	1024	Search completed: Augus: Job time : 85.3499 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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August 19, 2003, 04:46:44; Search time 300.529 Seconds (without alignments) 7930.701 Million cell updates/sec
OM nucleic - nucleic search, using sw model
                                                            Run on:
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1 tctgagggaaacagtgactg......gtgacaacatgcgaccgtga 1065 1504479 segs, 1118970152 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 US-09-987-455-7 Scoring table: Perfect score: Sequence: Searched: Title:

Total number of hits satisfying chosen parameters:

3008958

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB e Maximum DB e

/cgm2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
/cgm2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
/cgm2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
/cgm2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
/cgm2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
/cgm2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
/cgm2\_6/ptodata/2/pubpna/US10B\_NEW\_PUB.seq:\*
/cgm2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
/cgm2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\* fptodata/2/pubpna/US09A\_PUBCOMB.seq:\* /ptodata/2/pubpna/US09B\_PUBCOMB.seq:\* /ptodata/2/pubpna/US09G\_PUBCOMB.seq: /ptodata/2/pubpna/US09\_WIRW\_PUB.seq:\* Cgn2 6/ptodata/2/pubpna/USO7 PUBCOMB.seq:\*
Cgn2 6/ptodata/2/pubpna/DECT NEW PUB.seq:\*
Cgn2 6/ptodata/2/pubpna/USO6\_NEW PUB.seq:\*
Cgn2 6/ptodata/2/pubpna/USO6\_NEW PUB.seq:\*
Cgn2 6/ptodata/2/pubpna/USO6\_NEW PUB.seq:\*
Cgn2 6/ptodata/2/pubpna/USO8
CGn2 Published\_Applications\_NA: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 1065 100.0 1065 11 US-09-987-455-7 2 1063.4 99.8 1689 9 US-09-987-455-7 4 1063.4 99.8 2509 14 US-10-193-66-7 5 1063.4 99.8 2519 9 US-09-969-271-6 6 1062 99.7 1128 11 US-09-987-455-2 7 1062 99.7 1128 11 US-09-987-455-2 8 1061.8 99.7 2641 10 US-09-987-455-2 10 191.6 18.0 1212 10 US-09-987-458-144 9 230.2 21.6 329 122 US-10-007-226A-433 11 185 17.4 1415 14 US-09-880-503-15 12 170.8 16.0 1475 10 US-09-880-776A-122 14 170.8 16.0 1475 10 US-09-880-776A-122 15 170.8 16.0 1475 11 US-09-880-776A-122 16 170.8 16.0 1475 11 US-09-880-778-122 16 170.8 16.0 1475 11 US-09-466-396A-122 16 170.8 16.0 1475 11 US-09-466-396A-122	Result No.	Score	Query Match	å Query Match Length DB	DB	ID	Description
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16.0 1475 11 US-09-466-396A-122 16.0 1475 12 US-10-117-982-122	14	170.8			10	US-09-897-778-122	Sequence 122, App
16.0 1475 12 US-10-117-982-122	15	170.8			11	US-09-466-396A-122	Sequence 122, App
	16	170.8		•	12	US-10-117-982-122	Sequence 122, App

61 CTCACCGAGTCGGGTGCCTCCTGCCTCCGTGGAATTCCATGATCCTGATAGGCAAGGTT 120

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Sequence 159, App	Sequence 458, App Sequence 1, Appli	Sequence 123, App	Sequence 123, App	Sequence 123, App		Sequence 123, App			Sequence 12, Appl	Sequence 160, App	183	Sequence 1989, Ap	14	Sequence 16, Appl	Sequence 10405, A	Sequence 743, App	4	Sequence 1, Appli	Sequence 552, App	1612	Sequence 18438, A	Sequence 11188, A	Sequence 237, App	Sequence 237, App	Sequence 12715, A	Sequence 35, Appl
US-10-101-510-159 US-09-971-392-46	US-10-101-510-458 US-10-076-421-1	US-09-735-705-123	US-09-850-716A-123	US-09-897-778-123	US-09-466-396A-123	US-10-117-982-123	US-10-101-510-383	US-09-864-761-1682	US-09-880-503-12	US-10-301-822-160	US-10-171-311-183	US-10-106-698-1989	US-09-880-503-14	US-09-880-503-16	US-09-918-995-10405	US-10-101-510-743	US-10-101-510-448	US-09-858-909-1	US-09-954-456-552	US-09-880-107-1612	US-09-864-761-18438	US-09-918-995-11188	US-09-920-300A-237	US-10-033-528-237	US-09-918-995-12715	US-09-879-792-35
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2336	2336 1296	2294	2294	2294	2294	2294	2344	474	1236	2304	2304	2486	831	972	461	1959	2035	2048	2036	2036	116	457	372	372	442	1230
16.0	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.6	15.6	15.6	15.6	15.2	15.0	15.0	13.1	11.5	11.5	11.5	. 11.3	11.3	10.7	6.6	8.7	8.7	8.3	7.9
170.8	167.6	167.6	167.6	167.6	167.6	167.6	167.6	166	166	166	166	162	159.8	159.8	139	123	123	123	120.4	120.4	114.4	105	92.4	92.4	88	83.8
118	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	c 42	c 43	44	45

## ALIGNMENTS

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APPLICANT: Artaly manostoi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz

TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT APPLICATION NUMBER: 08/09/987,455
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: GB 0027779.8
PRIOR FILING DATE: 2000-11-14
SROR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence: coding ; OTHER INFORMATION: sequence for K2S protein US-09-987-455-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                   Sequence 4, Application US/09987455 Publication No. US20030049729A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100. Matches 1065; Conservative
                                                                                                        APPLICANT: Aranya Manosroi
US-09-987-455-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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COGGGTGGTCCTCGCGAGGAGGAGCAGAATTTGAA 540 셤 ò ద

RESULT 2
US-09-987-455-7
Sequence 7, Application US/09987455
Publication No. US20030049729A1
'GENERAL INFORMATION:

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; Publication No. US20030096733A1
; GENERAL INFORMATION:
; APPLICANT: WY. TOT
; APPLICANT: LI, Jinan
; TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
; FILE REFERENCE: 3810/1J577-US3
; CURRENT APPLICATION NUMBER: US/10/193,656
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/304,461
; PRIOR APPLICATION NUMBER: US 60/304,490
; PRIOR PILING DATE: 2001-07-10
; PRIOR PELING DATE: 2001-07-10
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; Patent No. US20020098179A1
; GENERAL INFORMATION:
; APPLICANT: Fitzer Inc. (All designated States except GB and EP (GB));
; APPLICANT: Fitzer Limited (GB and EP (GB) only);
TITLE OF INVENTION: Pharmaceutical Combinations
; TITLE OF INVENTION: Pharmaceutical Combinations
; FILE REFERENCE: PCS10951APME
; CURRENT APPLICATION NUMBER: US/09/969,271
; CURRENT APLICATION NUMBER: GB 0025473.0
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PRACESO for Windows Version 4.0
; SEQ ID NO 6
                                                                                                                                       AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGCCCCCAGGCAAACTTGCACGACGCC
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                                                                                    TACGGCAAGCATGAGCCTTGTCTCTTTCTATTCGGAGCGGCTGAAGGAGCTCATGTC
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Pred. No. 0;
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Best Local Similarity 99.9
Matches 1064; Conservative
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; ORGANISM: Homo sapiens
US-09-969-271-6
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                                                  TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCATGACTTTGGTG
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; Patent No. US20020098179A1
; Patent No. US20020098179A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc. (All designated States except GB and APPLICANT: Pfizer Limited (GB and EP (GB) only)
; TITLE OF INVENTION: Pharmaceutical Combinations
; PILE REFERENCE: PCS10951APME
; CURRENT APPLICATION NUMBER: US/09/969,271
; CURRENT APPLICATION NUMBER: GB 0025473.0
; PRIOR APPLICATION NUMBER: GB 0025473.0
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5: 7
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Best Local Similarity 99.9%;
Matches 1064; Conservative 0
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ORGANISM: Homo
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                                                                         PUBLICATION INFORMATION:
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RELEVANT RESIDUES: (1)..(2509)
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 SOFTWARE: Patentin version
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Publication No. US20030049729A1

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APPLICANT: Friedrich Goetz

APPLICANT: Friedrich Goetz

TITLE OF INVENTION: Methods for Large Scale Production of Recombinant

TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules

FILE REFERENCE: 0652.2190001

CURRENT APPLICATION NUMBER: 08/09/987,455

CURRENT FILING DATE: 2001-11-14

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NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

TTENDY II.128

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OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CB1
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APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REPERENCE: PA.0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR APPLICATION NUMBER: 60/238,331
SEQ.ID NOS: 194
SEQ.ID NOS: 194
SEQ.ID NO 144
SEQ.ID NO 144
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Pred. No. 0;
0; Mismatches
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; Patent No. US20020156263A1
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Matches 1063; Conservative
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LOCATION: 2635
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                                                                                                                                   APPLICANT: Jiradej Manostori
APPLICANT: Jiradej Manostori
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Rolf-Guenther Werner
ITILE OF INVENITON: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                            Sequence 5, Application US/09987455
Publication No. US20030049729A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 1062; Conservative
                                                                                                    GENERAL INFORMATION:
APPLICANT: Aranya Manosroi
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OTHER INFORMATION: 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)
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APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: GING ARRAYS OF CANDIDATE GENES
FILE REFREENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT ELLING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 433
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Pred. No. 4.3e-63;
0; Mismatches 6; Indels 0;
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US-10-007-926A-433
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Best Local Similarity 97.5%;
Matches 232; Conservative
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LOCATION: (57)
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NAME/KEY: modified_base
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NAME/KEY: modified_base
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ORGANISM: Homo sapiens
FEATURE:
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Sequence 15, Application US/0980503

Patent No. US20020131964a1

GENERAL INFORMATION:
GENERAL INFORMATION:
FILLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILLE REFERENCE: 9596-331

CURRENT APPLICATION NUMBER: US/09/880,503

CURRENT FILING DATE: 2001-06-13

Sequence 433, Application US/10007926A Publication No. US20030143539A1 GENERAL INFORMATION: APPLICANT: BERTUCCI, FRANCOIS APPLICANT: HOULGATTE, REMI APPLICANT: BIRNBAUM, DANIEL

US-10-007-926A-433

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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youdyao
APPLICANT: Wang, Youghao
APPLICANT: Wang, Youbyao
APPLICANT: Wang, Youbu
APPLICANT: Stainman, Kathleen
APPLICANT: Stainman, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14004
SOFTWARE FEELSE FEELSE FOR WINDOWS VERSION 4.0
                                                                                                                                                             GACTGGAATTGTGAGCTGGGCCGTGGATGTGCCCTGAAGGACAAGCCAGGCGTCTACAC
                                                                 1026 TTCCTGCCAGGAGACTCAGGGGACCCCTCGTCTTTCCCTCCAAGGCCGCATGACTTT
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Publication No. US20030099974A1
GENERAL INFORMATION:
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US-09-735-705-122
is Sequence 122, Application US/09735705
patent No. US20020052329A1
general information:
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NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 1414, 1415
OTHER INFORMATION: n = A,T,C or
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Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGAAGCTGATTTCCCACCGGGAGTGTCAGCAGCCCCACTACGGCTCTGAAGTCAC 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGA 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507 CAGGAGGCACCGGGGGGCTCTGTCA---CCTACGTGTGTGGAGGCAGCCTCATCAGCCC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGGGTTTCCGCCCCACCACCTGAC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGCTCTTCAGCTGGGGCTGGGGAACATAATTACTGCAGGAACCCAGACAACCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCG
                                                                                                                                                                                                                                                                                                                         CAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGGAGTACTGTGATGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 TGACTGCGCAGATGGAAAATTAAAATTTCAGTGTGCCCAAAAGACTCTGAGGCCCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGCATCAAAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAATTTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624 CGTCTACCTGGGTCGCTCAAGGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGT
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                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                               Length 1212,
                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                               Score 191.6; DB 10; Length
Pred. No. 1.5e-50;
0; Mismatches 459; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 CTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCA---
       60/212,847
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 1212
                                                                                                                                                                                                                                  18.0%;
                                                                                                                                                                                                                               Query Match 18.0
Best Local Similarity 52.3
Matches 549; Conservative
                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-503-15
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1023 119

963

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1064 TCCGGAGCAGCTGAAGATGACTGTTGTGAAGCTGATTTCCCACCGGGAGTGTCAGCAGCC 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1226 TTCCCTCCAAGGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGCCCT 1285
                                                                                                                                                                 1004 GTTTGGCACAAGCTGTGAGAFCACTGGCTTTGGAAAAGAGAATTCTACCGACTATCTCTA 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    933 TCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            criderargadededariedreaerrrrracedadaaaaegeedageaergacaeradegeee 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 GCCCTGCCTGCCCTGGAACTCTGCCACTGTCCTTCAGCAAACGTACCATGCCCACAGATC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 TGATGCTCTTCAGCTGGGCCTGGGGAACATAATTACTGCAGGAACCCAGACAACCGGAG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 GCGACCCTGGTGCTATGTGCAGGTGGGCCTAAAGCCCCTTGTCCAAGAGTGCATGGTGCA
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  633 TGCCCAGGAGCAGCGTGGTCCGCACTGTGCCTTCCCCCGGCGGACCTGCAGCTGCC
                                                     TTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACA
                                                                                                                                                                                                                                                                                                                                813 ACATTTACTTTACAGAACAGTCACCGACAACATGCTGTGTGTTGGAGACACTCGGAGCGG
                                                                                                              GGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCTTTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGCCCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCCTGGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGGACAAGCCACGCGTCTACACGAGAGTCTCACACTTCTTACCCTGGATCCG 1339
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Sequence 122, Application US/09850716A

Patent No. US20020115139A1

GREREAL INFORMATION:

APPLICANT: Kalos, Michael D.

APPLICANT: Reter, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

CURRENT PRILIG DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 122

LENGTH: 1475
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16.0%; Score 170.8; DB 10;
Best Local Similarity 51.3%; Pred. No. 7e-44;
Matches 551; Conservative 0; Mismatches 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCCTGCTCCACCTGCGCCTGAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-850-716A-122
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US-09-850-716A-122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACACAGCACAGAACCC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587 CCAAAAGACTCTGAGGCCCCGCTTTAAGATTATTGGGGGAGAATTCACCACCATCGAGAA 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA-----CTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCCCTG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 CAGTGCCCAGGCACTGGGCCTGGCCAACATAATTACTGCCGGAATCCTGATGGGGATGC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 CAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 CTCCTGCTCCACCTGCGCCTGAG---- 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCGGGGCATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTGGAGGCAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCATTGA 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             647 ccascccrestrrscssccarcrassassascacsscs---sascrcrercaccracer 703
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                                                                                             APPLICANT: Banger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stair A.W.
APPLICANT: Stair A.W.
APPLICANT: Stair A.W.
APPLICANT: Stair A.W.
APPLICANT: Handerson, Robert A.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21011.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
NUMBER OF SEQ ID NOS: 419
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Pred. No. 7e-44;
0; Mismatches 457; Indels 66;
                                                                         Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
Henderson, Robert A.
McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 51.3%;
Matches 551; Conservative (
                                                     Kalos, Michael D.
Wang, Tongtong
Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Homo sapien
US-09-735-705-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 122
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NUMBER OF SEQ ID NOS: 467
SOFTWARE: EstSEQ for Windows Version 4.0
SEQ ID NO 122
LENGTH: 1475
                                                                  TYPE: DNA
ORGANISM: HOMO
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    DB 10; Length 1475;
Score 170.8; DB 10; Length
Pred. No. 7e-44;
0; Mismatches 457; Indels
  Query Match
Best Local Similarity 51.3%;
Matches 551; Conservative
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APPLICANT: Mainerakis, Margarita
APPLICANT: Banger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS:AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455016
CURRENT APPLICATION NUMBER: US/09/897,778

CURRENT FILING DATE: 2001-06-28

APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick

GENERAL INFORMATION:

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Pred. No. 7e-44;
0; Mismatches 457; Indels
                                                                                                                                                                                                                                               APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C4
CURRENT APPLICATION NUMBER: US/09/466,396A
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FeatSEQ for Windows Version 3.0
SEQ ID NO 122
LENGTH: 1475
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                                                                                                                                                                                                    Sequence 122, Application US/09466396A Publication No. US20030119763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 51.3%;
Matches 551; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-09-466-396A-122
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Search completed: August 19, 2003, 14:22:30 Job time : 302.529 secs

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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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BX329047 BU149958 BX389609 BU146167

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11111111111111111111111111111111111111	RESULT 1 BX3.29047/C LOCUS DEFINITION ACCESSION VERSION VERSION VERSION VERSION VERSION VERFERENCE ONGANISM TITLE JOURNAL COMMENT

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/seve_"maxe | /seve_"dorsal root ganglia" | /seve_"type="adult, 36 yr" | /lab_host="adult, 36 yr" | /lab_host="adult, 36 yr" | /lab_host="adult, 36 yr" | /lab_host="bliow." | /lab_host=| /lab_hos
                                                                                                                                                                                                                                                                                                                                                                                      BU149958 1137213 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone_IMAGE:6184119 5', mRNA sequence.
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                                                                                                                       88 AACATGCTGTGTGCTGGAGAGACACTCGGAGCGGCGGCGCCCCAGGCAAACTTGCACGACGCC 29
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 912)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Linn at:
http://image.llnl.gov
Ridhy sequence start: 18
High quality sequence start: 18
High quality sequence stop: 644.
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80.1%; Score 853; DB 13;
Best Local Similarity 98.9%; Pred. No. 5.4e-212;
Matches 901; Conservative 0; Mismatches 5;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:6184119"
                                                                                                                                                                                                    TGCCAGGGGGATTCGGGAGGCCCCC 925
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.larity 98.6%; Pred. No. 5.7e-223;
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cne.fr, Web: www.genoscope.cns.fr
was normalized Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4498.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eqe=CSOBAF025ZGO9_AF02376_3&cluster=4498.r.
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAF025ZGO9_AF02376_3.
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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                                          CAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCTGGCAGGCTGCCATCTTTGCCAA
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/organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="CS0DI039YK15"

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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                   79.9%; Score 850.6; DB 13; Length 962; 96.4%; Pred. No. 2.3e-211; tive 0; Mismatches 30; Indels 3;
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 891;
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EST 08-MAY-2003

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

 (bases 1 to 962)

Homo sapiens (human)

EST

KEYWORDS

DEFINITION

ACCESSION

VERSION

Homo sapiens

ORGANISM

REFERENCE

120

255

9

375 240 435

180

555

495

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BQ278177 993 bp mRNA linear EST 07-MAY-2002 AGENCOURT_7061709 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5805153
                                                                                                                                                                                                                                                                                       CCCTCCTGCTCCACCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAGGA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AGGTCGCCCGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGTGGTTGT 300
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                                                                                                                                            136 CCCAGTGCCCAGGCACTGGGCCTGGGCAACATAATTACTGCCGGAATCCTGATGGGGAT
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                                                                                                          Gaps
                                                                                                      5
                                                                      891;
                                                                      Length
                                                                                                        Indels
                                                                    DB 13;
                                                                                                          14;
                                                                    Score 818.6; DB 13.
Pred. No. 5.2e-203;
0; Mismatches 14;
                 176
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                 b
                 271
Technologies.
                                                                    76.9%;
                 266 c
                                                                                     Best Local Similarity 98.2
Matches 849; Conservative
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/dev_stage="adult, 36 yr"
/lab_host="antub"
/lab_host="antub"
/clone_lupski dorsal root ganglion"
/clone_lupski dorsal root ganglion"
/clone_lupski dorsal root ganglion"
/clone="vector: pcMv-spopre" (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT.priming.
Directionally cloned using the following adaptors:
5.-TCGACCACGCCTCG-3; and
5.-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BU146167
AGENCOURT 7981262 Lupski dorsal root ganglion Homo sapiens cDNA clone IMAGE:6185661 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                        GGCTGTGGACAGAAGGATGTCCCGGGTGTGTACAAAAGGTTACCAACTACCTAGACTGG 1041
                                                                                                                                                                                                780
                                                                                                                                                                                                                                                            CCCTGGTGTGTCTGAACGATGCGCGCATGACTTTGGTGGGCATCATCAGCCTGGGCCTG 840
                                  720
                                                                                                                                                         ACTCGGAGCGGCGGGCGAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGC 921
                                                                                                                                                                                                                                    CCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCCATCATCAGCTGGGGCCTG 981
                                                                                                                                                                                                                                                                                                                                            841 GCTGTGGAACAGAAGATGTCCCGGTTGTTCCCACCAAG--TTACCACTTACTAAACTGG 898
                 801
                                                                                       TGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGAC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 891)

MH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Context: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clond clarribution: MGC clone distribution information cloud through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13576 row: m column: 22
High quality sequence stop: 665.
                                                                                                          TCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 þe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6185661"
                                                                                                                                                                                                                                                                                                                                                                                1042 ATTCGTGACAACATGCGACCGTGA 1065
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BU146167.1 GI:22659699
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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BU146167
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_tref="texton:9606"
/clone="type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/tlone="type="ductal carcinoma, cell line"
/tlone="type="ductal carcinoma, cell line"
/tlone lib="NHH MGC_ll0"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGGGG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ690978 8046707 NIH_MGC_110 Homo sapiens CDNA_clone IMAGE:62091205', mRNA sequence.
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      360 CATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGAGCAGCGTGGT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 883)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                   480 CICCGGCTACGGCAAGCATGAGGCCTTGTCTCTTTTTTCGGAGCGGCTGAAGGAGGC
                                                                                                                                                                                                                                                                                                                              540 TCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTACTTAACAGAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGACGCCTGCCAGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGAC
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                                                                                                                   CTCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGC
                                                                                                                                                                                                                                                                                             TCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGT
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2367 row: o column: 09
High quality sequence stop: 658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/mol_type="mRNA"

/mol_type="mRNA"

/db_txef="texacon:9606"

/clone="type="texacoarcinoma, cell line"

/tissue_type="texacoarcinoma, cell line"

/tissue_type="texacoarcinom
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                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 993)
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Contact: Robert Strausberg, Ph.D.
Email: Gapba-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llh.gov
Plate: LLCM2043 row: o column: 10
High quality sequence stop: 681.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                      BQ278177.1 GI:20488385
EST.
                                                                                                                sapiens (human)
mRNA sequence.
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Craniata; Vertebrata; Eutele Catarrhini; Hominidae; Homo

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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedax - France
Bmail: sequrefégenoscope.cns.fr waw.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
A498.r. For more information about this cluster, see
http://www.genoscope.nns.fr/
cgi-bin/cluster.cgi?seq=CSOBAF025ZG09_AF02376_2&cluster=4498.r.
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAF02ZG09_AF02376_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol type="maxon:9606"
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/clone="CSODI039YR15"
/tissue type="HACENIRA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENIRA COT 25-NORMALIZED"
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/clone libt strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched with a NotI-oligo(dT)
grimer. Five prime end enriched with Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
a 273 c 264 g 186 t 6 others
                                                            Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Butheria; Primates; Catarrhini; Hor
11 (bases 1 to 918)
11, W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length, cDNA libraries and normalization
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                         sapiens (human)
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0; Mismatches 8;
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Matches 816; Conservative
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                                                                                        ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACGCA
                                             Gaps
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75.8%; Score 807.6; DB 13; Length 918; 96.4%; Pred. No. 4e-200; ive 0; Mismatches 29; Indels 3;
                        Best Local Similarity 96.4
Matches 855; Conservative
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BX389608
BX389608 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI039YK15 5-PRIME, mRNA sequence.
BX389608.1 GI:30463469

DEFINITION ACCESSION VERSION

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888 bp mRNA linear EST 04-SEP-2002
AGENCOURT 8043192 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6084476
5., mRNA sequence.
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/ AD LYPE="MRNA"

/ AD XTEF="Laxon:9606"

/ Clone="INAGE:6578533"

/ Lissue type="teratocarcinoma, cell line"

/ Lissue type="teratocarcinoma, cell line"

/ Lissue type="teratocarcinoma, cell line"

/ Lissue type="teratocarcinoma"

/ Lissue type
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18 I (Bases I to 930)

19 NIH-MGC http://mgc.nci.nih.gov/.

10 Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 639.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       TGA-CTTTGGTGGGCATCATCAGCTGGGG-CCTGGGCTGTGGACAGAAGGATGTCCCGGG 1007
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AGENCOURT_10412263 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6578533 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 916)

2 National Eutelia; Primates; Catarrhini; Hominidae; Homo.

3 National Institutes of Health, Mammalian Gene Collection (MGC)

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-r@mail.nih.gov

7 Tissue Procurement: Life Technologies, Inc.

6 Contact: Robert Strausberg, Ph.D.

7 Tissue Procurement: Life Technologies, Inc.

6 Contact: Robert Strausberg, Ph.D.

7 Tissue Procurement: Life Technologies, Inc.

6 Contact: Robert Strausped by: The I.M.A.G.E. Consortium (LIML)

7 DNA Sequencing by: Incyte Genomics, Inc.

7 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

8 Rute: LiAML1476 row: k. column: 09
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  GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCCAGGAGAGCAGCGTG
                         GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCCCCTGTGCCCAGGAGAGCGTG
                                                                                  GTCCGCACTGTGTGTCCCCTTCCCCCGGCGGACCTGCCACTGCCGGACTGTGAG
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/tissue type="ductal carcinoma, cell line"
/tasue type="ductal carcinoma, cell line"
/lab host="Dulb [phage-resistant)"
/clone lib="NIH MGC 110"
/clone lib="NIH MGC 110"
/note="Crgan: pancreas; Vector: pOTB7; Site_1: Xhol;
Site_2: BcoR1; cDNA made by oligo-dr priming
Directionally cloned into EccR1/Xhol sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 888)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/MOL_type="mRNA"
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// Ab_type="laxge cell carcinoma"
// Alab_host="MRNA"
// Alab_host="DH10B (phage-resistant)"
// Alab_host="Mage-resistant"
// Alaboratory of Gerald M. Rubin (University of California, Berkeley)
// Alaboratory of Gerald M. Rubin (University of California, Berkeley)
// Alaboratory of Gerald M. Rubin (University of California, Berkeley)
// Alaboratory of Gerald M. Alabora
                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2550 row: p column: 02
High quality sequence start: 35
High quality sequence stop: 684.
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                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (Dases 1 to 950)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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98.1%; Pred. No. 4.9e-189;
ive 0; Mismatches 13; Indels
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/organism="Homo sapiens"
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Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library." 272~c~256~g~18\overline{4}~t
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/tissue type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
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/note="Organ: pancreas; Vector: pOTB7; Site_1: Xho1;
Site_2: BcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE616613 948 bp mRNA linear EST 24-AUG-2000 601278864F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611007 5', mRNA sequence.
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                                                                              TCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACCTT 642
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 948)
WIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                GCTGTGCCCAGGAGCAGCGTGCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGC
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                                                             TGCCGGACTGGACGGAGTGTGAGCTCCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTT
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov p column: 16 High quality sequence start: 2 High quality sequence stop: 759.
High quality sequence stop: 759.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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671 658 715

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772 850 832

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BUYSOU216 974 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8945604 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6459629
5', mRNA Bequence.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 974)
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 492 TCCTGCTGGATTCTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCTGCCCACCTG
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2645 row: a column: 06
High quality sequence stop: 603.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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/lab host="DHIOB (phage-resistant)"
/clone_lib="NIH MGC_49"
/note="Organ: sKih, Vector: pOTB7, Site 1: XhoI, Site 2:
BCORI; CDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACAAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
ILRT (Life Technologies). Note: this is a NIH_MGC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 958)
WIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                           Email: cgapbe-remail.nih.gov
Tissue procurement: ATCC/DCTP/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 810.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Euteleostomi;

Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelé Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 709)

BE732704.1 GI:10146696 Homo sapiens (human) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection

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// Along in placenta; Vector: poTB7; Site\_1: Xho1;
// Along in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
// Along and Superscript II RT (Life Technologies)." ä 556 919 120 376 GETCGCCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCATCATCATCTGGATTCTCT 240 360 TCCATAAGGAATTTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAAT 420 CCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGC 256 436 496 CTGCCGCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAGACGTGATCTTGGGCA 300 GGCTCTTCGCCCACCATCGCCTCCCACCCCTGGCAGCTGCCATCTTTGCCAAGCACAGGA 180 9 CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM752 row: d column: 17
High quality sequence start: 3
High quality sequence stop: 701. cercerecrecerecescereasacagracasecesecereasirrescareaaasaas GGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAGCACAGGA GAACATACCGGGGTCCCTGGCGAGGAGGAGCAGAAATTTTGAAGTCGAAAAATACATTG TCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAAT ccaagcccrggracacgrgcrgaagaaccgcaggcrgacgrgaggagracrgrgargrgc GGTCGCCCGGAGAGCGGTTCCTGTGCGGGGCATACTCATCAGCTCCTGCTGGATTCTCT CTGCCGCCCACTGCTTCCAGGAGGTTTCCGCCCCCACCACCTGACGGTGATCTTGGGCA Gaps 1; DB 10; Length 709; Indels 65.1%; Score 693.4; DB 10 99.7%; Pred. No. 2.5e-170; iive 0; Mismatches 1; 1. .709 /organism="Homo sapiens" Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC Location/Qualifiers Query Match
Best Local Similarity 99.,
-hes 705; Conservative 197 -257 61 317 121 377 181 437 241 497 301 557 361 BASE COUNT ORIGIN FEATURES a ઠે

> BE732704 LOCUS DEFINITION RESULT 15

ACCESSION

709 bp mRNA linear EST 15-SEP-2000 601571366F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3925600 5', BE732704

617 CGGATTCGTCCCCTGTGCCCAGGAGCAGCGTGGTCCGCACTGTGTGTG	421 GGATTCGTCCCGCTGTGCCCAGGAGAGCGTGGGTCCGCACTGTGTGCCTTCCCCCGG 480	677 CGGACCTGCAGCTGCACTGGACGGAGTGTGAGCTCTCCGGGCTACGGCAAGCATGAGG 736	481 CGGACCTGCAGCTGCCGGACTGGAGTGTGAGGTCTCCGGCTACGGCAAGCATGAGG 540	737 CCTIGITCTTTTCTATTCGGAGGGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCA 796	541 CCTTGICCCCTTTCTATTCGGAGCTGAAGGAGGCTCATGTCATG	797 GCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACAGGTGCTG 856	601 GCCGCTGCACATCACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGCTG 660	857 GAGACACTCGGAGCGGCGCCCCCAGGCAAACTTGCACGACGCCTGC 903	661 GAGACACTCGGGGGGGGGGCCCCCGGCCAACTTGCACGACGCCTGC 706	
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US-09-987-455-4 1065 1 tctgagggaaacagtgactg.....gtgacaacatgcgaccgtga 1065 Scoring table: . IDENTITY\_NUC Gapext 1.0 Title: Perfect score: Sequence:

2888711 segs, 20454813386 residues Searched:

5777422 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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2. gb\_htg:\*

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Pred. No. is the number of results predicted by chance to have a

Goetz,F., Werner,R.G., Tayapiwatana,C., Manosroi,A. and Manosroi,J. Methods for large scale production of recombinant dna-derived tpa or k2s molecules Patent: WO 0240650-A 4 23-MAY-2002;

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Db   724 TACGGCAAGCATGTCTCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTC 783	193 193 193 193 193 193 193 193 193 193	CC topology: Linear; CC hypothetical: No; CC hypothetical: No; CC hypothetical: No; CC hypothetical: No; CC resurce: clone=pTTkPAdeltatrp; FH Key Location/Qualifiers  1. 1068 FT CDS /product='t-PA'. FT CDS /product='t-PA'.  1. 1068
1068 bp DNA US 5840533.  ci,H., Hayashi,M. Aator 24-NOV-1998; fiers nown" 13 g 215 t Score 1065; DB Pred. No. 4.7e-2	1 TCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCAC	1

LOCUS LOCUS LOCUS LOCUS LOCUS DEPINITION DNA sequence of coding region in pmTTk. A27727 VERSION VERSION A27727  VERSION A27727  VERSION A27727  VERSION A27727  VERSION A27727  A27727	Query Match 100.0%; Score 1065; DB 6; Length 1170; Best Local Similarity 100.0%; Pred. No. 4.8e-248; Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 TCTGACGGAAACAGTGACTGCTACTTTCGGAATGGGTCAGCCTACCGTGGCACGCAGC 60	0y 61 CTCACCGAGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTT 120	OY 121 TACACAGACACAGAACCCCAGGCACAGGCCTGGGCCAAACATAATTACTGCCGG 180	OY 181 AATCCTGATGGCGAAGCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG 240	Oy 241 GAGTACTGTGATGTGCCCTCCTGCTCCGGGCCTGAGACAGTACAGCCAGC	Oy 301 TITCGCATCAAAGAAGGCTCTTCGCCGACACCTCCCCCCCCTGGCAGGCTGCCATC 360	Qy         361         TITGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGATACTCAGC         420           Db         466         TITGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGATACTCATCAGC         525	QY         421 TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCGGAGGGTTTCCGCCCACCACCTG 480           Db         526 TCCTGCTGGATTCTCTCTGCCGCCACTGCTTCCAGGAGGTTTCCGCCCCACCACCACCACCACCACCACCACCACCACCACC	QY         481 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGAGGAGGAGGAATTTGAA 540           DD         586 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGGAGAATTTGAA 645	QY         541 GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG         600	QY 601 CTGCTGCAGATCGGATTCGTCCCGCTGTGCCCAGGAGAGCGGGTCCGCACT 660 
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661 GTGTGCCTTCCCCCGGCGGCGCCTGCCGGCTGCCGGAGTGTGAGCTCTCCGGC 720

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946 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGCCCCAGGCAAACTTGCACGACGCC 1005
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                                                                                                   286 AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACGCAGGCTGACGTGG
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                                                                                                                                                                                                                                         121 TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG
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                                                                                                                                                             CTCACCGAGTCGGGTGCCTCCTGCTGGAATTCCATGATCCTGATAGGCAAGGTT
                                                                                                                                                                                                                                                                                                                      181 AATCCTGATGGGGATGCCCAAGCCCTGGTGCCACGTGAAGAACCGCAGGCTGACGTGG
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                                                                                1 TCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACAGGC
Length 1170;
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                                       Indels
                    4.8e-248;
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  DB 6;
t; Score 1065; D
t; Pred. No. 4.8e
0; Mismatches
  100.0%;
100.0%;
  Query Match
Best Local Similarity 100.
Matches 1065; Conservative
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NOVEL TISSUE PLASMINOGEN ACTIVATION FACTOR
PATENT: JP 1989104167-A 12 21-APR-1989;

FUJISARA PHARMACEUT CO LTD
OS Artificial gene
OC Artificial gene
OC Artificial sequence; Genes.

PN 1989104167-A/12

PD 21-APR-1989

FF 01-AUG-1988 JP 1988192320

PR 01-AUG-1987 GB 87 8718298, 26-OCT-1987 GB 87 8725052, PR
13-NOV-1987 GB 87 8726633

PI NWA MIREO, SAITO YOSHIMASA, SASAKI HITOSHI, HAYASHI MASAKO,
PI NOTANI JOJI,
PC C12N9/64,C12N1/20,C12N5/00,C12N15/00//A61K37/54,(C12N9/64, PC
C12N1-19),
CC strandedness: Double;
CC topology: Linear;
CC anti-sense: No;
CC anti-sense: No;
FF Key Location/Qualifiers
FT CDS
FT
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                                             TACGGCAAGCATGAGGCCTTGTCTTTTCTATTCGGAGCGCGCTGAAGGAGGCTCATGTC
                                                                  TACGGCAAGCATGAGGCCTTGTCTTTTTTTCGGAGCGGCTGAAGGAGGCTCATGTC
                                                                                                                         AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
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JP 1989104167-A/12.
Synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 1170)
Niwa M., Saito, Y., Sasaki, H., Hayashi, M., Notani, J. and
Kobayashi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
338 c 346 g 237 t

    11.1170
/product='new
Location/Qualifiers

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Synthetic DNA encoding E01945
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Synthetic DNA encoding new t-PA tissue plasminogen activator.
E01937
                                                                                                                                                                                                                          1090 AACATGCTGTGTGTGTGGAGACACTCGGAGCGGGGGGCCCCAGGCAACTTGCACGGCC 1149
                                                                                                                                                                                                                                                                                 1150 TGCCAGGGCATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG 1209
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  721 TACGGCAAGCATGAGGCCTTGTCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTC
                                                                                                                                                                         1030 AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
                                                            910 GTGTGCCTTCCCCCGGGGGACCTGCAGCTGCAGATGAGAGTGTGAGCTCCCGGC
                                                                                                                   970 TACGGCAAGCATGAGGCCTTGTCTCTTTTTCGGAGGGGCTGAAGGAGGCTCATGTC
                                                                                                                                                                                                                                                                  901 TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCATGACTTTGGTG
                                            661 GIGIGCCIICCCCCGGCGGACCIGCAGCIGCCGGACIGGACGGAGTGIGAGCTCTCCGGC
                                                                                                                                                        781 AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
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anti-sense: No;
*source: clone=pTQkPAdeltatrp;
Location/Qualifiers
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Location/Qualifiers
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hypothetical: No;
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1 (bases 1 to 1314)

Nwa,M., Salto,Y., Sasaki,H., Hayashi,M., Notani,J. and Kobayashi,M.
Now tissue plasminogen activator
New tissue plasminogen activator
Patent: EP 0302456-A 35 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD

Location/Qualifiers
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1126 GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1170
                                                                            A27435 1314 bp DNA linear DNA sequence of coding region in pTQkPAdeltatrp. A27435
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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synthetic construct
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I (bases I to 1419)
Niwa, M., Salto, Y., Sasaki, H., Hayashi, M., Notani, J.
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NDA sequence of coding region in pmTQk112.
A27725 A27725.1 GI:21727236
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon;32630"
413 c 426 g 271 t
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Patent: BP 0302456-A 49 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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/mol_type="genomic DNA"
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OY 541 GTCGAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG 600	OY 601 CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCCAGGAGAGCGGGGTCCGCACT 660	Qy         661         GTGTGCCTTCCCCCGGCGGAACCTGCAGCTGCAGAACTGGAACTGTGAGCTCTCCGGC         720           Db         1015         GTGTGCCTTCCCCCGGCGGACCTGCCGGACTGGACGGAGTGTGAACGTCTCCGGC         1074	Oy 721 TACGGCAAGCATGAGGCTTGTCTCTTTTGGAGGGGCTGAAGGGGGCTCATGTC 780	OY 781 AGACTGTACCCATCCAGCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC 840	Qy         841 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCCGCCCAGGCAAACTTGCACGACGC         900           Db         1195 AACATGCTGTGTGCTGGAGAGACACTCGGAGCGGCCCCCAGGCAAACTTGCACGACGC         1254	OY 901 TGCCAGGCGATTCGGGAGGCCCCTGGTGTGTTCGAACGATGGCCGCATGACTTTGGTG 960	OY 961 GGCATCATCAGCTGGGGCCTGGGGCTGTGGACAAGGATGCTCCGGGTGTGTACACAAAG 1020	OY 1021 GTTACCAACTACCTAGACTTCGTGACAACATGCGACCGTGA 1065 	RESULT 11 AR05996 AR059996 1419 bp DNA linear PAT 29-SEP-1999	AR059996 1 GI:5986446 intrace	NISM Unknown. Unclassified.  Unclassified.  Upases 1 to 1419)	AUINORS NYWAYN, SAICO,I., SABARI,H., HAYABNI,M., NOCANI,U. AND KODAYABNI,M. TITLE Tissue plasminogen activator JOURNAL Patent: US 5840533-A 62 24-NOV-1998; FRAMTHER	ĭ E	Query Match 100.0%; Score 1065; DB 6; Length 1419; Best Local Similarity 100.0%; Pred. No. 4:8e-248; Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 355	61 CTCACCGAGTGGCTGCCTCCTGCCTCGTGGAATTCCATGATCCTGATAGGCAAGGTT	UY 121 TACACAGAGACCCCAGGCCCAGGCCTGGGCCTGGGCAAACATAATTACTGCCGG 180  Db 475 TACACAGCACAGAACCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG 534

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Unclassified.

I (bases 1 to 1689)

Mulvihill, E.R., Nexo, B.A., Yoshitake, S., Ikeda, Y., Suzuki, S.,
Habhimoto, A. and Yusuriha, T.

Mutant t-PA with kringle replacement
Patent: BP 029934-A1 44 07-DBC-1988;

Location/Qualifiers
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llarity 100.0%; Pred. No. 4.8e-248;
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Best Local Similarity 100.0%; Pred. No. 4.8e-248;
Matches 1065; Conservative 0; Mismatches 0;
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Mulvihill,E.R., Nexo,B.A., Yoshitake,S., Ikeda,Y., Suzuki,S.,
Hashimoto,A. and Yuzuriha,T.
Mutant t-PA with kringle replacement
Patent: EP 0293934-Al 46 07-DEC-1988;
Location/Qualifiers
j. 1689 Gaps ö Length 1689; Indels Score 1065; DB 6; Pred. No. 4.8e-248; 0; Mismatches 0; 324 /organism="unknown" 484 c 504 g 100.08; Best Local Similarity 100.0%; Matches 1065; Conservative 377 a 721 1345 ò g ò 윤 8 02-DEC-1994 PAT

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1689 bp 1 EP 0293934.

46 from Patent GI:590640

Sequence 4 I06614 I06614.1

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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RESULT 14 106614

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Bollen, A.J., Gheysen, D., Jacobs, P., Pierard, L. and Collen, D.J.
Patent: WO 8804690-A 3 30-JUN-1988;
Location/Qualifiers
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Search completed: August 19, 2003, 04:46:33 Job time : 4473.78 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic -	OM nucleic - nucleic search, using sw model
Run on:	August 18, 2003, 19:51:53; Search time 375.192 Seconds (without alignments) 7662,485 Million cell undates/sec
Title:	115-09-987-455-4

US-09-987-455-4 1065 1 tctgagggaaacagtgactggtgacaacatgcgaccgtga_1065	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	2552756 segs, 1349719017 residues	Total number of hits satisfying chosen parameters: 5105512
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	<pre>2: /sibsi/gegdata/geneseq/geneseqn-embi/NA1981.DA1:* 3: /SIDS1/gegdata/geneseq/geneseqn-embi/NA1982.DAT:*</pre>	<pre>5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:* 6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*</pre>	7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*	8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*	<pre>10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*</pre>	11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*		13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*	gcgdata,	15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*	17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*	19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*	20: /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*	21: /SIDS1/gcgdata/geneseq/genesegn-emb1/NA2000.DAT:*	22: /SIDS1/gcgdata/geneseg/genesegn-embl/NA2001A.DAT:*	23: /SIDS1/gcgdata/geneseg/genesegn-embl/NA2001B.DAT:*	24: /SIDS1/gcgdata/geneseg/genesegn-emb1/NA2002.DAT:*	25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human kringle 2 se Sequence of coding Sequence of coding Sequence of coding Sequence of coding Novel plasminogen Tissue plasminogen
SUMMARIES .	AADGOGIG AAN91120 AAN91123 AAN91133 AAT27588 AAT27587 AAR82178
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% Query re Match Length DB	1065 1068 1170 1314 1419 1680 1680
% Query Match	1000.001
Score	1065 1065 1065 1065 1065 1065
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Sequence encoding	placmid nomila one	Flasmid psiliz end Human tPA clone	Human tissue plasm	Sequence encoding	Plasmid pKG12 cont	Entire sequence of	Plasmid pEMp1-tPA.	Glycosylated plasm	Sequence encoding	Sequence encoding	Tissue plasminogen	Mutated t-PA analo	tPA024	Part of tPA023 gen	Sequence encoding	T-PA67+ mutant wit	Human tissue plasm	Full-length tissue	Human tissue plasm	Sequence encoding	T-PA variant contg	Plasmid plgNTQTPA	T-PA with -ve char	Sequence encoding	Human tissue plasm	Plasmid plgN delta	cDNA sequence enco		Human tissue plasm	Human tissue type	Sequence encoding	DHFR/intron (WTras	OmpA-K2S fusion pr	Sequence encoding	Sequence of coding
AAQ01358	AMORESS	AA087370	AAV37294	AAN60659	AAN90542	AAN70491	AAN81970	AAQ03581	AAQ11550	AAQ11551	AAN82179	AAN81090	AAQ04903	AAQ04904	AAQ05177	AAQ13379	ABK52546	AAT27585	AAZ31998	AAN60700	AAQ12073	AAQ05534	AAQ12072	AAN70248	AAQ86576	AAQ05535	AAN60146	AAN90508	ABK52545	ABL59544	AAN30001	AAT15930	AAD40614	AAQ06762	AAN91122
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## ALIGNMENTS

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Tissue plasminogen activator; tPA; kringle 2 serine protease; stroke; K2S; cardiac infarction; acute myocardial infarction; pulmonary embolism; artery occlusion; deep vein thrombosis; blood clotting; thrombolytic; cerebroprotective; cardiant; ompA; enzyme; human; gene; ds.
                                                                                                                                                                                         Location/Qualifiers
1..1065
/*tag= a
/product= "Human K28 protein"
                                                                                     Human kringle 2 serine protease (K2S) DNA.
                      AAD40616 standard; DNA; 1065 BP.
                                                                                                                                                                                                                                                                                             07-NOV-2001; 2001WO-EP12857.
                                                                                                                                                                                                                                                                                                                    14-NOV-2000; 2000GB-0027779.
                                                                 30-OCT-2002 (first entry)
                                                                                                                                                                                                                                                   WO200240650-A2
                                                                                                                                                                   Homo sapiens.
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                                           AAD40616;
RESULT 1
AAD40616
ID AAD40
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CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGAGCAGCGTGGTCCGCACT
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87GB-0025052.
87GB-0026683.
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P-PSDB; AAP94407.
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26-OCT-1987;
13-NOV-1987;
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                                                                                                                                                              The present invention relates to a method of producing extracellularly accreed, active, correctly folded, recombinant tissue plasminogen activator (tPA), Kringle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants. Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vein thrombosis or related diseases associated with unwanted blood clotting. The present sequence
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                                                                         Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
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             Manosroi A;
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100.0%; Pred. No. 9.7e-237;
ive 0; Mismatches 0;
             Manosroi J,
             Tayapiwatana C,
                                                                                                                                        Claim 12; Page 31; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 1065; Conservative
             Goetz F,
                                    WPI; 2002-519376/55.
P-PSDB; AAE25036.
                                                                                                                peptide OmpA
             Werner R,
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longer half-life and stronger thrombolytic activity,
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Best Local Similarity 100.0%; Pred. No. 9.7e-237;
Matches 1065; Conservative 0; Mismatches 0;
                                                  (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
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coding region in plasmid pTQkPA

(updated)
(first entry)

Location/Qualifiers 1..1065 /\*tag= a

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Tissue plasminogen activator; tPA; thrombolytic agent;
plasminogen; vascular diseases.
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Kobayashi M;

Notani J,

87GB-0018298. 87GB-0025052. 87GB-0026683.

88EP-0112569

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                       Query Match 100.0%; Score 1065; DB 10; Length 1314; Best Local Similarity 100.0%; Pred. No. 1e-236; Matches 1065; Conservative 0; Mismatches 0; Indels 0;
Sequence 1314 BP; 286 A; 386 C; 393 G; 249 T; 0 other;
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AAN91123 standard; DNA; 1314

RESULT 4 AAN91123

25-MAR-2003

AAN91123;

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                                                                    Kobayashi
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                                                                                                                                                                                                                            Sequence 1419 BP; 309 A; 413 C; 426 G; 271 T; 0 other;
                                                                                                                         New tissue plasminogen activator - comprising finger and growth factor domains lacking longer half-life and stronger thrombolytic activity.
                                                                   <del>ن</del>
                                                                   Notani
                                                                                                                                                                                            field.)
                                                                                                                                                                                           (Updated on 03-OCT-2002 to add missing OS fie (Updated on 25-MAR-2003 to correct PA field.)
                                                                   Hayashi M,
                                                                                                                                                                      Disclosure; Page ?; 68pp; English
                                           (FUJI ) FUJISAWA PHARM CO LTD
87GB-0018298.
87GB-0025052.
87GB-0026683.
                                                                  Saito Y, Sasaki H,
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                                                                                      WPI; 1989-040625/06.
P-PSDB; AAP94416.
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03-AUG-1987;
26-OCT-1987;
13-NOV-1987;
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Matches 1065;
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841 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGCCCCAGGCAAACTTGCACGACGCC
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                   AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
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                                                                                          AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCC
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                                                                                                                                                                                                                                                                                                               Tissue plasminogen activator; tPA; alpha2-plasmin inhibitor; fibrinolytic; thrombolytic; fibrin; thrombosis; blood clotting; protein engineering; kringle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid plasminogen activator comprises human tPA activator and N-terminal crosslinking domain from alpha2-plasmin inhibitor useful to treat thrombosis and image blood clots
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92US-0827587.
94US-0254485.
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06-JUN-1994;
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06-AUG-1996
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of plasminogen replaces the native KI domain (AAR96221) of plasminogen replaces the native KI domain of tissue plasminogen activator (FPA) (AAR96220). It was obtd. by inserting a synthetic plasminogen KI domain DNA (AAT27586) into PPA cDNA and can be expressed in transformed Escherichia coli RRI cells (FERM P-9272). Novel plasminogen activators are produced that show increased clot lysing specificity or plasma half-life.
                                                                                                                                                                                                                                                                                                                                  ; Score 1065; DB 17; Length 1680;
; Pred. No. 1.1e-236;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                      Sequence 1680 BP; 387 A; 471 C; 479 G; 343 T; 0 other;
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976 TITGCCAAGACACAGAGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGC 1035
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                                DB 17; Length 1680;
                                                            Indels
     Sequence 1680 BP; 386 A; 471 C; 480 G; 343 T; 0 other;
                             Score 1065; DB 17;
Pred. No. 1.1e-236;
; Mismatches 0;
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                             ucuery match 100.0%;
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A DNA construct (AAT27587) codes for a novel plasminogen activator (AAR96223) in which the kringle K1 domain of plasminogen (see also AAR96221) is mutated to substitute asparagine for aspartic acid at position 5, and replaces the native K1 domain of tissue plasminogen activator (LPA) (AAR96220). It was obtd. by mutagenesis of the sequence in vector Zem99-8000 (see also AAT27587). The novel protein can be expressed in Escherichia coli RRI/Zem99-8010 cells protein can be expressed in Escherichia coli RRI/Zem99-8010 cells increased clot lyaing specificity or plasma half-life. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                        Tissue plasminogen activator; tPA; alpha2-plasmin inhibitor; fibrinolytic; thrombolytic; fibrin; thrombosis; blood clotting; protein engineering; kringle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybrid plasminogen activator comprises human tPA activator ar
N-terminal crosslinking domain from alpha2-plasmin inhibitor
useful to treat thrombosis and image blood clots
                                                                                                                                                        GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                             Novel plasminogen activator DNA.
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                                         181 AATCCTGATGGGGATGCCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG
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Plasmid encoding the modified tPA is 99-6300 and its transformant is E.coli RR1. Zem 99-6300 (FERM P-9127).
This modified tPA, used to treat thrombosis, is of high quality and has a longer half life period in blood.
See also AAW8217-N82179.
(Updated on 10-WAR-2003 to add missing OS field.)
(Updated on 25-WAR-2003 to correct PF field.)
(Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                              plasminogen activator; tPA; thrombosis; N-glycosylation;
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1.1e-236;
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Matches 1065; Conserv
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(updated)
(first entry)
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18-JUN-1990
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a positively charged amino acid. The resulting analogues are inserted
through the charged amino acid. The resulting analogues are inserted
through the charged in useful for the treatment of diseases or disorders
associated with the formation of thrombi in blood vessels e.g.
infarctions, thrombosis and embolism. The analogue, in the 1-chain form,
chibits the properties of a proenzyme; however on plasmin-catalysed
cleavage of the one-chain form, the activity of the 2-chain form is fully
tetained. Compared to native t-PA, it has a higher fibrin selectivity,
this results in a fibrinolytic agent with a higher fibrin selectivity,
as the fibrinogenolytic activity induced by the analogue is reduced
relative to that induced by native 1-chain t-PA.
(Updated on 25-MAR-2003 to correct PA field.)
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                 infarction treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tissue plasminogen activator (t-PA) analogue - with higher fibrin selectivity than native t-pa, useful for treating infarction, thrombosis and embolism
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Pred. No. 1.1e-236;
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0
             Wild type tissue plasminogen activator (t-PA);
thrombosis treatment; embolism treatment.
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100.0%; Pred. No. 1.-
0; Mismatches
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/note="synthetic 3' adaptor"
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/note="synthetic 5'
1738..1780
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1..123
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Matches 1065; Conservative
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P-PSDB; AAR04699.
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                                                                  Homo sapiens
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                                                                                                                                                      1489 AACATGCTGTGTGTGTGGAGACACTCGGAGCGGCGCGCCCCAGGCAACTTGCACGCCC
                                         1189 GTCGAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
                                                                                                                                  661 GIGIGOCTICCCCCGGCGGACCTGCAGCTGCAGCTGGAGTGTGAGCTCTCCGGC
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               GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
                                                                          CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTCCCCAGGAGCAGCCGCGCGCCCT
                                                                                                                                                                                                   TACGGCAAGCATGAGGCCTTGTCTCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTC
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                                                                                                                                                                                                                                              Σ
                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequence of native tPA gene is excised from plasmid pST112, digested with BamHI and SalI to form plasmid pST118. (Updated on 01-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                              Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2100;
                                                                                                                                                                                                                                                                                                                     New tissue plasminogen activator - comprising finger and growth factor domains lacking tPA for longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2100 BP; 498 A; 595 C; 597 G; 410 T; 0 other;
                                                                                                                                                                                                                                              Saito Y, Sasaki H, Hayashi M, Notani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 1065; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.1e-236;
Matches 1065; Conservative 0; Mismatches 0;
Location/Qualifiers
25..1710
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                   Example 29; Fig 21; 68pp; English.
                                                                                                                                                   87GB-0018298.
87GB-0025052.
87GB-0026683.
                                                                                                                                                                                                                (FUJI ) FUJISAWA PHARM CO LTD
                                                                                                                       88EP-0112569
                                                                                                                                                                                                                                                                       WPI; 1989-040625/06.
P-PSDB; AAP94406.
                                                                                                                                                   03-AUG-1987;
26-OCT-1987;
13-NOV-1987;
                                                                                                                     02-AUG-1988;
                                                                                        08-FEB-1989
                                                          EP302456-A
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                      1429 AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCCGAC
                                                                                           1489 AACATGCTGTGTGCTGGAGACACTCGGAGGGGGGGCCCCAGGCAAACTTGCACGACGCC
                                                                                                                                                       1549 TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG
                                                                                                                                                                                     GGCATCATCAGCTGGGGCCTGGGCTGTGGAAGGATGTCCCGGGTGTGTACACAAAG
      AGACTGTACCCATCCAGCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
                                                               841 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCC
                                                                                                                           TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG
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/*tag= a
/note= "Bignal sequence and finger-like domain"
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/product= Kringle-2 domain
973..2162
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/product= EGF-like domain
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                  tPA with N-terminal peptide of plasminogen linked is more stable in vivo than the native form. It is useful as a thrombolytic agent in the treatment of vascular diseases eg myocardial infarction,
                                          New tissue plasminogen activator - having N-terminal peptide of plasminogen linked to tissue plasminogen activator for increased stability in vivo.
                                                                                                                                                                                                                                                            DB 11; Length 2100;
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                                                                                                                                                                                                                            Sequence 2100 BP; 498 A; 595 C; 597 G; 410 T; 0 other;
                                                                                                                                                                                                                                                          Query Match 100.0%; Score 1065; DB 11; Best Local Similarity 100.0%; Pred. No. 1.1e-236; Matches 1065; Conservative 0; Mismatches 0;
                                                                                                                                                                                  pulmonary embolism etc. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                      Disclosure; Page ?; ?pp; English.
 1990-232757/31
WPI; 1990-232/5/
P-PSDB; AAR06237
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/note= "Kringle-2
973..2162
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/note= "catalytic
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                                             A cDNA clone of human tissue plasminogen activator (tPA) was amplified by PCR using the primers given in AA087366-69. The amplified tPA DNA (AAQ87370) was ligated into vector KS+ to obtain plasmid TPA-KS+. The construct was used in combinatorial methods involving RNA splicing-mediated shuffling of tPA domains implasmid pinvl (AAQ87347) to generate novel tPAs having limproved thrombolytic properties.

(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                 Sequence 2162 BP; 520 A; 606 C; 619 G; 417 T; 0 other;
                                                                                                                                                                                                                                                   Query Match
100.0%; Score 1065; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.1e-236;
Matches 1065; Conservative 0; Mismatches 0; 1
                Example 4; Page 59-60; 87pp; English
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Reverse splicing construct containing fragments of autocatalytic introns - able to cleave and ligate discontinuous nucleic acid for generating new genes and e.g. ribozymes, libraries of enzymes and antibodies finger-like domain" Plasmid pINVI; reverse-splicing intron; group II intron; exon binding site; domain W motif; branch site acceptor; nucleophilic group; transesterification; phosphodiester bond autocatalytic Y-branched intron; reverse splicing reaction; GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065 duman tissue plasminogen activator gene sequence. Location/Qualifiers
82..334
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335..447
/\*tag= b /note= "EGF-like domain"
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/\*tag= c /note= "Kringle-1 domain"
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AAN60659 Btandard; DNA; 2547 BP.
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The present sequence represents the human tissue plasminogen activator gene. It was used to construct plamsid TPA-KS+, which is used in the countries of the invention. The specification describes a purified reverse oblicing intron which comprises a segment comprising a reverse-splicing intron which comprises a segment comprising a raturally present in the intron and a second segment comprising a naturally present in the intron and a second segment comprising a retargetor, and a nucleophilic group for transesterifying a phosphodiester bond of an RNA. Together the two segments form an applicable of an expense splicing reaction the first segment into substrate RNA by a reverse splicing reaction. The reverse-splicing introns are used, by specific cleavage and ligation of discontinuous nucleic acid, to generate new genes and gene products, e.g. ribozymes (for use in gene therapy or as reagents in DNA manipulation, e.g. replacements for restriction enzymes) or immunologically active or signal-transducing proteins such as antibody
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Location/Qualifiers
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           AAP60790). Also new (3) microorganisms
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                                                              Sequence 2547 BP; 627 A; 688 C; 691 G; 541 T; 0 other;
position 276 is replaced (275 and 276 refer to the in the mature protein; i.e. AAS 310 and 311 of AAS (1) DNA sequences; (2) expression vectors; and (3) and cell cultures transformed with these vectors. (Updated on 25-MAR-2003 to correct PR field.)
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llarity 100.0%; Pred. No. 1.1
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Larity 100.0%; Pred. No. 1.1e-236;
Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                       Sequence 2560 BP; 634 A; 690 C; 689 G; 547 T; 0 other;
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	121 TACACAGCACAGAACCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG 180 	181 AATCCTGATGGGGATGCCAAGCCCTGGTGCTGAAGAACCGCAGGTGAGTGG 240	241 GAGTACTGTGATGTGCCCTCCTGCTCCACCTGAGACAGTACAGCCAGC	360	361 TTTGCCAAGAGAGGTCGCCCGAAGAGCGGTTCCTGTGCGGGGCATACTCAGC 420 	421 TCCTGCTGGATTCTCTCTGCCGCCACTGCTTCCAGGAGAGTTTCCGCCCCACCACCTG 480	481 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGGAGAAATTTGAA 540 	541 GTCGAAAATACATTGTCCATAAGAATTCGATGATGACACTTACGACAATGACATTGCG 600 	601 CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCGGGGTCCGCACT 660 	661 GIGIGCTICCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGC 720 	721 TACGGCAAGCATGAGGCCTTGTCTCCTTTCGAAGGGGCTGAAGGAGGCTCATGTC 780	781 AGACTGTACCCATCCAGCCGCTGCACATTTACTTAACAGAACAGTCACCCGAC 840 	δ н	96 16	961 GGCATCATCAGCTGGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG 1020 	21 GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065	179
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	Description	Sequence 44, Appl	62,	10,	42,	3, 7	Sequence 3, Appli	25	64,	48,	. 52(	Sequence 39, Appl	Patent No. 5344773	Sequence 1, Appli	H	Sequence 46, Appl	20	38	52,	54	7	6	6	99	Sequence 1, Appli	26		Sequence 5, Appli
SUMMARIES	ID	US-08-811-949-44	US-08-811-949-62	US-08-814-412-10	US-08-811-949-42	US-08-119-512-3	US-08-488-015B-3	US-08-488-015B-25	9-6	US-08-811-949-48	5200340-1	US-08-883-795A-39	5344773-1	US-08-286-740-1	PCT-US95-09576-1	US-08-811-949-46	US-08-811-949-50	US-08-811-949-38	US-08-811-949-52	US-08-811-949-54	US-08-137-116-2	US-09-553-498-9	US-09-618-869-9	US-08-811-949-66	US-08-427-640-1	US-08-811-949-56	5223256-3	US-08-427-640-5
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Sequence 58, Appl Sequence 3, Appli Sequence 60, Appl Patent No. 5185259 Sequence 7, Appli Sequence 5, Appli Sequence 6, Appli Patent No. 5244676 Sequence 40, Appl Patent No. 5200340 Patent No. 5200340 Sequence 122, Appli Sequence 122, Appli	
US-08-811-949-58 US-08-427-640-3 US-08-811-949-60 5185-259-2 US-08-427-640-7 US-08-558-269-5 US-09-410-882-5 5244676-4 US-08-811-949-40 5200340-3 US-07-957-039A-7 US-09-643-5397-122 US-09-643-615A-122 US-09-542-615A-122 US-09-542-615A-122	
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## ALIGNMENTS

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Sequence 44, Application US/08811949

Patent No. 5840533

GENERAL INFORMATION:
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: MASAKA
APPLICANT: HAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKO
APPLICANT: TISSUB PLASMINOGEN ACTIVATOR
ITILE OF INVENTION: TISSUB PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: DELON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                    US-08-811-949-44
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RESULT 1
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100.0%; Score 1065; DB 2; Length 1068;

Query Match

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Sequence 62, Application US/08811949
Patent No. 5840533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1419 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 703-413-300
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                      ZIP: 22202
COMPUTER READABLE FORM:
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Matches 1065; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY:
, LOCATION:
US-08-811-949-62
                                          RESULT 2
US-08-811-949-62
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               Indels
  1.4e-291;
              0; Mismatches
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 Pred.
100.08;
Best Local Similarity 100.
Matches 1065; Conservative
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                                                                                                                                                                          GENERAL INPORMATION:
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI MASAKO
APPLICANT: HORASHI MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1419;
1024 GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
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llarity 100.0%; Pred. No. 1.5e-291;
Conservative 0; Mismatches 0;
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414 120 474 180 534 240 594

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996 TTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATC 1055
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,412
FILING DATE: 11-MAR-1997
CLASSIFICATION: 435
ATCORNEY AGENT INPORMATION:
NAME: Jarrell Ph.D., Brenda H.
REGISTRATION NUMBER: 0079571-0040
TELEPENONE: 617 248 4000
TELEPENONE: 617 248 5000
TELEPENONE: 617 248 5000
TELEFAX: 617 248 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1065; DB 3; Best Local Similarity 100.0%; Pred. No. 1.7e-291; Matches 1065; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                               CLONE: amplified t-PA clone -08-814-412-10
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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TITLE OF INVENTION: Intron-Mediated Techniques and Reagents
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Chate, Hall & Stewart
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STREET: 53 State Street
CITY: Boston
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Patent No. 6150141
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-814-412-10
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iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 1065; Conservative
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                                                                                                      TACGGCAAGCATGAGGCCTTGTCTCTTTCTATTCGGAGCGCTGAAGGAGGCTCATGTC
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT NOWBER: US/08/811,949

FILING DATE: 05-MAR-1997

CLASSIFICATION NUMBER: US/08/811,949

FLING DATE OF COMPATION:

NAME: OBLON, NORMATION:

REFERENCE/DOCKET NUMBER: 18-966-0

TELEFRAX: 703-413-3220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANICON: TISSUE PLASMINOGEN ACTIVATOR
ANDER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1755 S. JEPFERSON DAVIS HIGHWAY, SUITE CITY: ARLINGTON
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-811-949-42
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                                                                                                                                   766 CTCACCGAGTCGGGTGCCTCCTGCGTGGAATTCCATGATCCTGATAGGCAAGGTT
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                                                                                                              61 CTCACCGAGTCGGGTGCCTCCTGCCTCCGTGGAATTCCATGATCCTGATAGGCAAGGTT
                                                                                                                                                                                       121 TACACAGCACAGAACCCCCAGTGCCCAGGCACTGGGCCTGGGCCAAACATAATTACTGCCGG
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     Mismatches
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     Matches 1065; Conservative
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GGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG 1020
                          1609 GGCATCATCAGCTGGGGCTGTGGCTGTGGAAGGATGTCCCGGGTGTGTACACAAAG
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                                                                                                                                                                                           Sequence 3, Application US/08119512
Patent No. 5498531
GENERAL INFORMATION:
TITLE OF INVENTION: INTRON MEDIATED RECOMBINANT TECHNIQUES
TITLE OF INVENTION: AND REAGENTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                        GTTACCAACTACCTAGATTCGTGACAACATGCGACCGTGA 1065
                                                                                             1669 GITACCAACTACCTAGACTGGATTCGTGACAACATGCGACGTGA 1713
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LOCATION: 335..447
OTHER INFORMATION: /product= "EGF-like domain"
FEATURE:
NAMB/KEY: misc_feature
LOCATION: 448..714
OTHER INFORMATION: /product= "Kringle-1 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 973.72162
; OTHER INFORMATION: /product= "Catalytic domain"
US-08-119-512-3
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LOCATION: 82.334
OTHER INDORMATION: /product= "Signal So
OTHER INFORMATION: Pinger-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,512
FILING DATE: 10-SEP-1993
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HUI-008
TELEFRAN: (617) 227-7400
TELEFRAN: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: ODDLOGY: both
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                   STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
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LOCATION: 715..972
OTHER INFORMATION: /product=
FEATURE:
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Best Local Similarity
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NAME/KEY: 1
LOCATION:
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RESULT 7
US-08-488-015B-25
; Sequence 25, Application US/08488015B
; Eatent No. 5780772
; GENERAL INFORMATION:
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100.0%; Score 1065; DB 1; Length 2162;
Best Local Similarity 100.0%; Pred. No. 1.8e-291;
Matches 1065; Conservative 0; Mismatches 0; Indels 0;
                                                             APPLICANT: Jarrell, Kevin A.
TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
TITLE OF INVENTION: AND REAGENTS
WUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: 82..334
OTHER INFORMATION: /product= "Signal Sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 335..447
OTHER INFORMATION: /product= "EGF-like domain"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 448._714
OTHER INFORMATION: /product= "Kringle-1 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 715. 972
OTHER INFORMATION: /product= "Kringle-2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: 973.2162
OTHER INFORMATION: /product= "Catalytic domain"
                                                                                                                                                                                                                          COUNTY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,015B
FILING DATE: 07-UNW-1995
ATTORNEY/AGENT INPORMATION:
NAWE: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELECHONE: (617) 832-1000
TELECHONE: (617) 832-1000
TELECHONE: (617) 832-1000
SELECTALION INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH 2162 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5780272
OTHER INFORMATION: Finger-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: both
MOLECULE TYPE: other nucleic acid
                                                                                                                                                   E: Foley, Hoag & Eliot
One Post Office Square
              Sequence 3, Application US/08488015B
Patent No. 5780272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: 715..972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                             GENERAL INFORMATION:
                                                                                                                                                                STREET: One PORTY: BOSTON STATE: MA
                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-488-015B-3
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                                                                                   121 TACACAGCACAGAACCCCCAGTGCCCAGGCACTGGGCCTGGGGCAAACATAATTACTGCCGG
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APPLICANT: SATTO, VOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HAYASHI, MASAKAZU
APPLICANT: NOTANI, JOUJI
APPLICANT: ROBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STRRET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APERICAL NELSON NELSON
SOGTWARE: PatentIn Release #1.0, Version #1.30
SOGTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR.1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 64, Application US/08811949; Patent No. 5840533; GENERAL INFORMATION:
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                            RECOMBINANT TECHNIQUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPERENCY/DOCKET NUMBER: HUV-008.02
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
                                                                                                 ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MS
COUNTRY: USA
ZIP: O2109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,015B
FILING DATE: 07--UNV-1995
ATTORNEY/AGENT INFORMATION:
APPLICANT: Jarrell, Kevin A.
TITLE OF INVENTION: INTRON-MEDIATED
TITLE OF INVENTION: AND REAGENTS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, Hoad & Elict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear / MOLECULE TYPE: CDNA US-08-488-015B-25
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1066 GGCATCATCAGCTGGGGCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG 1125
886 AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC 945
                                                                                                                                              1006 TGCCAGGGCGATTCGGGAGGCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG
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                                                                      946 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCC
                                                                                                          901 TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG
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Pred. No. 4.2e-291;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                          GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA 1065
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, MASAKAZU
APPLICANT: NOTANI, MASAKAZU
CORRESPONDENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: AALINGTON STATE: VA
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MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLEASIFICATION: 45
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 US-08-811-949-48
; Sequence 48, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
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Best Local Similarity 99.9%;
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TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION
                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                         99.8%;
                            TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 base pairs
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Matches 1064; Conservative
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; LOCATION:
US-08-811-949-64
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RESULT

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; APPLICANT: FOSTER, DONALD C.; MULVIHILL, BILEEN R.; O'HARA,
; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINGEN TCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCG1 Indels Score 1063.4; DB 6. Pred. No. 4.8e-291; 0; Mismatches 1; NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987 99.8%; Similarity 99.9%; 781 g ઠ

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1615 TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG 1674
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                                                                                                               1135 TCCTGCTGGATTCTCTCTCTGCCGCCCACTGCTTCCAGGAGGGTTCCGCCCCACCACCTG
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                      AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG
                                                                                                                                                                       TITICGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATC
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TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGG
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APPLICANT: WEI, CHA-MER.HSIUNG, NANCY,REDDY, VERWURI B.;
LEMONTT, JEFFREY F.,DACKOWSKT, WILLIAM,DOUGLAS, RICHARD;
COLE, EDWARD S.,PINCELL, JR., RICHARD D.,LAU, DAVID TAL-YUI
TITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN
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  AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGCCCCAGGCAAACTTGCACGACGCC
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US-08-883-795A-39

Sequence 39, Application US/08883795A

Patent No. 5985607

GENERAL INFORMATION:

APPLICANT: Delcuve, Genevieve

APPLICANT: Awang, Gregor

TITLE OF INVENTION: Recombinant DNA Molecules and Expression

TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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STREET: 40 King Street West
CITY: Toronto
COUNTRY: Toronto
COUNTRY: 10 King Street West
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN 1997
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REGISTRATION NUMBER: 40,261
RELEFAK: (416) 364-7311
TELEFPHONE: (416) 364-7311
TELEFAK: (416) 361-1398
INPORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LEMGTH: 1955 base pairs
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Best Local Similarity 99.9%;
Matches 1064; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-08-883-795A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                      TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG
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99.9%; Pred. No. 8.7e-291;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS. SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/286,740
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                            US-08-286-740-1

US-08-286-740-1

Sequence 1, Application US/08286740

PATEMEN INFORMATION:

APPLICANT: Crowley, Craig W.

TITLE OF INVENTION: METHOD FOR SELEC

TITLE OF INVENTION: HOST CELLS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE.

CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 99.9
64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
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Pred. No. 5.5e-291;
0; Mismatches 1;
; ACTIVATOR PRODUCED BY RECOMBIANT DNA
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/782,686
; FILING DATE: 01-OCT-1985
; APPLICATION NUMBER: 656,770
; APPLICATION NUMBER: 656,770
; PILING DATE: 01-OCT-1984
                                                                                                                                                                                         99.8%;
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Best Local Similarity 99.9
Matches 1064; Conservative
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GENERAL INFORMATION:
APPLICANT: GENERYECH, INC.
TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
TITLE OF INVENTION: HOST CELLS
INTHER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Best Local Similarity 99.9%; Pred. No. 8.7e-291;
Matches 1064; Conservative 0; Mismatches 1;
                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09576
                    Blvd
                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILOR APPLICATION DATA:
PILING DATE: 08-20G-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REPERBRICH DOCKNATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 411/225-1994
STREET: 460 Point San Bru:
CITY: South San Francisco
STATE: Californ'
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                          99.7%; Score 1061.8; DB 2; Length 1068; 99.8%; Pred. No. 1.1e-290; ive 0; Mismatches 2; Indels 0;
                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
         INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
703-413-3000
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                        1..1065
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1063; Conserv
TELEPHONE:
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                                                                                                                                                                                      LOCATION:
US-08-811-949-46
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GENERAL INFORMATION:

APPLICANT: NIWA, MINEO

APPLICANT: SAITO, YOSHIMASA

APPLICANT: ARASKI, HITOSHI

APPLICANT: HAYASHI, MASAKO

APPLICANT: HAYASHI, MASAKAZU

TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHMAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PELLCATION NUMBER: US/08/811,949
FILING DATE: 05-WAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-811-949-46
Sequence 46, Application US/08811949
; Patent No. 5840533
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841	844	901	904	961	964	1021	1024	ch complet	time : 84
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August 19, 2003, 04:46:44; Search time 300.529 Seconds (without alignments) 7930.701 Million cell updates/sec
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Compugen Ltd.
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                                                                                                                                                                                                                1504479 seqs, 1118970152 residues
GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                    Sequence:
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                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Sequence 4. Appli	Sequence 7, Appli	Sequence 6. Appli	Sequence 7. Appli	Sequence 5, Appli	Sequence 2. Appli	Sequence 5. Appli	Sequence 144. App	Sequence 433, App	Sequence 15, Appl	Sequence 12748, A	Sequence 122, App		122,	122,	Sequence 122, App
		ID	US-09-987-455-4	US-09-987-455-7	US-09-969-271-6	US-10-193-656-7	US-09-969-271-5	US-09-987-455-2	US-09-987-455-5	US-09-974-298-144	US-10-007-926A-433	US-09-880-503-15	US-10-198-846-12748	US-09-735-705-122	US-09-850-716A-122	US-09-897-778-122	US-09-466-396A-122	US-10-117-982-122
			11	11	0	14	6	11	11	10	12	10	14	6	10	10	11	12
		Match Length DB	1065	1065	1689	2509	2519	1128	1128	2641	329	1212	1415	1475	1475	1475	1475	1475
df	Query	Match	100.0	100.0	8.66	8.66	8.66	99.7	7.66	99.7	21.6	18.0	17.4	16.0	16.0	16.0	16.0	16.0
		Score	1065	1065	1063.4	1063.4	1063.4	1062	1062	1061.8	230.2	191.6	185	170.8	170.8	170.8	170.8	170.8
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Sequence 159, App Sequence 46, Appl Sequence 16, Appl Sequence 123, App Sequence 16, App Sequence 148, App Sequence 148, App Sequence 148, App Sequence 52, App Sequence 11, Appl Sequence 15, App Sequence 11, Appl Sequence 15, App Sequence 1612, App Sequence 1	Sequence 11188, A Sequence 237, App Sequence 237, App Sequence 12715, A
US-10-101-510-159 US-09-971-392-46 US-10-101-510-458 US-10-076-421-1 US-09-735-705-123 US-09-850-776A-123 US-09-850-776A-123 US-09-864-761-1682 US-10-117-982-123 US-10-117-982-123 US-09-884-761-1682 US-09-886-503-12 US-09-880-503-14 US-10-101-510-488 US-09-880-503-14 US-09-880-503-14 US-09-980-503-14 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-107-1612 US-09-880-107-1612	US-09-918-995-11188 US-09-920-300A-237 US-10-033-528-237 US-09-918-995-12715 US-09-879-792-35
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## ALIGNMENTS

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61 CTCACCGAGTCGGGTGCCTCCTGCCTCCGTGGAATTCCATGATCCTGATAGGCAAGGTT 120
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                                                                                                          APPLICANT: diradej Manosroi
APPLICANT: diradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT APPLICATION UNMER: US/09/987,455
CURRENT PILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-01-14
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100.0%; Pred. No. 0;
tive 0; Mismatches
                 Sequence 4, Application US/09987455 Publication No. US20030049729A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
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Matches 1065; Conservative
                                                                                                APPLICANT: Aranya Manosroi
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LENGTH: 1065
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US-09-987-455-4
US-09-987-455-4
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ANT: Aranya Manosroi ANT: Jiradej Manosroi ANT: Chatchai Tayapiwatana ANT: Riedrich Goetz ANT: Rolf-Guenther Wenner CANT: Rolf-Guenther Wenner OF INVENTION: Methods for Larg OF INVENTION: Methods for Larg OF INVENTION: NAB-Derived tPA REFERENCE: 0652.2190001 RT APPLICATION NUMBER: US/09/98' RT FILING DATE: 2001-01.11.14 APPLICATION NUMBER: 60/268,574 PILING DATE: 2001-02.05	PRIOR APPLICATION VMDER: GB 0027779.8  PRIOR FILING DATE: 2000-11-14  NUMBER OF SEQ ID NOS: 25  SOFTWARE: Patentin Ver. 2.1  SEQ ID NO 7  LENGTH: 1065  TYPE: DNA  TY	DEMATION: DE CAMATION: BE	AACAGTGACTGCTACTTTGGG	61 CTCACCGAGTGCGTGCTCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTT	QY         121 TACACAGCACAGAACCCCAGGGCCTGGGCCTGGGCAACATAATTACTGCCGG 180           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db	301 TTTCGCATCAAAGGAGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATC	31	Db 421 TCCTGCTGCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCTG 480  Qy 481 ACGTGATCTTGGGCAGAACATACCGGGTGGTCCCTCGCGAGGAGCAGCAGAAATTTGAA 540  L	541 GTCGABABATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG [	541 GICGAGAAAIIACAIIGICAIIAAGAAIILGAIGAIGACACIIACGACAAAIIGACAIIGCG 601 CIGCIGCAGCIGAAAICGGAIICGICCCGCIGIGCCCAGGAAGAGCAGCGIGGICCCCCACII
	Db   241	361 TTTGCCAAGCACGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCTACTCATCAGC 421 TCCTGCTGGATTCTCTGCCGCCCACTGCTTCCAGAGAGGTTTCCGCCCCACCACGG 421 TCCTGCTGGATTCTCTGCCGCCCACTGCTTCCAGAGAGGTTTCCGCCCCACCACGG 421 TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGAGAGGTTTCCGCCCCACCCCGCCCCCGCCCCCCCC	QY         481 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCCAGGAGCAGAAATTTGAA 540           DD         481 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAA 540		Db         601         CTGCTGCAGCTGAAATCGGGATTCGTCCCCGGCTGTGCCCAGGAGGGGGGGG	QY         721 TACGGCAAGCATGAGCCTTGTCTCCTTTCTATTCGGAGCGCCTGAAGGAGGCTCATGTC 780           Db         721 TACGGCAAGCATGAGGCCTTGTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTC 780           QY         781 AGACTGTACCCATCCAGCACATGACAACATTACTTAACAGAACAGTCACGGAC 840		841 AACATGCTGTGTGGTGGAGACACTGGAGGGGGGGGGGGG	961 GGCATCATCAGCACCTGGGCTGTGCACAGAAGGATGTCCCGC 1	GTTACCAACTACCTAGATTCGTGACAACATGCGACCGTGA 106	RESULT 2 US-09-987-455-7 ; Sequence 7; Application US/09987455

RESULT 2
US-09-987-455-7
Sequence 7, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:

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                                                 925 TTTCGCATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATC
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Publication No. US20030096733A1

GENERAL INFORMATION:
APPLICANT: NY. Tor
APPLICANT: HOLMDAHL, Rikard
TITLE OF INVENTION:
FILER REFERENCE: 3810/1J577-US3
CURRENT APPLICATION NUMBER: US/10/193,656
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/60/304,461
PRIOR APPLICATION NUMBER: US 60/304,461
PRIOR APPLICATION NUMBER: US 60/304,490
PRIOR PILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-13
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; Parent No. US20020098179A1
; GENERAL INFORMATION.
; APPLICANT: Pfizer Inc. (All designated States except GB and EP (SP)
; APPLICANT: Pfizer Limited (GB and EP (GB) only)
; TITLE OF INVENTION: Pharmaceutical Combinations
; TITLE OF INVENTION: PARENCE: US/09/969, 271
; CURRENT APPLICATION NUMBER: US/09/969, 271
; PRIOR PILING DATE: 2000-10-17
; PRIOR PILING DATE: 2000-10-17
; NUMBER: OF SEQ ID NOS: 7
; SOFTWARE: FREEESE for Windows Version 4.0
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99.8%; Score 1063.4;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 0; Mismatches
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CORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 2509

TYPE: DN

ORCANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank / X07393

RELEVANT RESIDUES: (1)..(2509)
US-10-193-656-7
                                                                                                               Score 1063.4;
Pred. No. 0;
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Best Local Similarity 99.9%;
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SOFTWARE: PatentIn
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; Patent No. US20020098179A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc. (All designated States except GB and
; APPLICANT: Pfizer Inc. (All designated States except GB and
; APPLICANT: Pfizer Inmited (GB and EP (GB) only)
; TITLE OF INVENTION: Pharmaceutical Combinations
; FILE REFERENCE: PCS10951APWE
; CURRENT APPLICATION NUMBER: US/09/969,271
; CURRENT FILING DATE: 2001-10-01
; PRIOR PILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
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ive 0; Mismatches
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	67 TCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCAC	61 CTCACCGAGTCGCTCCTCCCTCCCGTGGAAITCCATGATCCTGATAGGCAAGGTT 120	CTCACCGAGICGGCTCCTGCCTCCCGTGGAATTCCATGAICCTGATAGGCAAGGTT 1	TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCCAAAATAATTACTGCCGG 18	187 TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGGCGG 246 181 AATCCTGATGGGAATGCCAAGCCCTGGTGCCAAGGAGAAACGCGAGGCTGACGTGG 240	ATCCTGATGGGGGATGCCAAGCCCTGGTGCCTGCTGAAGAACCGCAGGCTGACGTGG 30	241. GAGTACTGTGATGTGCCTCCTGCTCCTGCGGCCTGAGACAGTACAGCCAGC		301 TITCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCCCCTGGCAGGCTGCCATC 360		427 TTTGCCAAGCACAGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGC 486	TCCTGCTGGTGGATTCTCTCTGCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCCACCTG	54		541 GTCGAAAATACATTGTCCATAAGGAATTCGATGATGACTTACGACAATGACATTGCG 600		CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACT	661 GIGIGCTTCCCCGGGGGACCTGCAGCTGCAGACTGGAGTGTGAGCTCTCCGGC 720	721 TACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTC 780	AGACTGTACCCATCCAGCCGCTGCACATCAACATTTACTTAACAGAACAGTCACCGAC 84		841 AACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGCCCCAGGCAAACTTGCACGACGCC 900	AACATIGCTIGTIGCTIGGAGACACTICGGAGCGGCGGGGCCCCCAGGGCAAACTTIGCACGACGCC · 9	901 TGCCAGGGCAFTCGGGAGGCCCCTGGTGTCTGAACGATGGCCGGATGACTTGGTG 960	1 GGCATCATCAGCTGGGGCCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG 102		1021 GTTACCAACTACCTAGACTTCGTGACAACATGCGACCG 1062 	
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Db 1181 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAAATTTGAA 1240	Qy 541 GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG 600	Db 1241 GTCGAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG 1300	601 CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCGGCGTGGTCCGCGT 66	1301	Oy         661         GRETGCCTTCCCCGGCGGACCTGCACTGCACTGGACGGACTGTGAGCTCTCCGGC         720           Db         1361         GTGTGCCTTCCCCGGCGAACTGCTGCACGGACTGCAGGAGTGCTCCACC         1420	TACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGGGGGGGG	Db 1421 TACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTC 1480	OY 781 AGACTGTACCCATCCACCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC 840	1481 AGACTGTACCAGCCGCTGCACATCACAACATTAACTTAACAGAACAGT	QY         841 AACATGCTGTGTGTGCTGGAGACACTCGGAGCGGGCCCCAGGCAACTTGCACGACGC 900	Qy 901 TGCCAGGGGATTCGGAAGGCCCCTGGTGTCTGAACGATGGCCGCATGACTTTGGTG 960	1601 TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCATGACTTTGGTG 1	UY 501 GOOD TATACHAGU 1020  DD 1661 GGCATCATCAGGGGCTGGGGCTGTGGACAGAGGATGTCCCGGGGTGGTACACAGAGGTGGTACAGAGGTGGTACAGAGGGTGGTACAGAGGGTGGTACAGGAGGTACAGGAGGATGTCCCGGGGTGGTACACCAGAGGTACACCAGGAGGATGTACACCAGGAGGTACACCAGGAGGATGTCCCGGGGTGGTACACCAGGAGGATGTCCAGGAGGATGTCCAGGAGGATGTACACCAGGAGGATGTACACCAGGAGGATGTACACCAGGAGGATGTACACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGATGACCAGGAGGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGA		Db 1721 GTTACCAACTACCTAGACTGGATTCGTGACAACAATGCGACCGTGA 1765	RESULT 6 11S-09-987-455-2	; Sequence 2, Application US/09987455 ; Publication No. US20030049729A1	APPLICANT: Aranya Manosroi ; APPLICANT: Jiradej Manosroi ; APPLICANT: Chatchai Tayapiwatana	<pre>; APPLICANT: Friedrich Goetz ; APPLICANT: Rolf-Guenther Werner ; TITLE OF INVENTION: Methods for Large Scale Production of Recombinant ; TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules</pre>	FILE REFERENCE: 0652.2190001 CURRENT APPLICATION NUMBER: US/09/987,455	; CURRENT FILING DATE: 2001-11-14 ; PRIOR APPLICATION NUMBER: 60/268,574 ; PRIOR FILING DATE: 2001-02-15	FRIOR APPLICATION NUMBER: GB 0027779.8 FRIOR FILING DATE: 2000-11-14 FIRER FOR SEC ID NOS: 25	SOFTWARE Patentin Ver. 2.1	; SEQ 1D NO 2 ; LENGTH: 1128 ; TYPE: DNA	) ORGANISM: Artificial Sequence ; FEATURE:	<ul> <li>OTHER INFORMATION: Description of Artificial Sequence: coding</li> <li>OTHER INFORMATION: sequence for OmpA-K2S fusion protein</li> <li>US-09-987-455-2</li> </ul>	Query Match 99.7%; Score 1062; DB 11; Length 1128; Best Local Similarity 100.0%; Pred. No. 0;	Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG 666
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CB1
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Fatent No. US20020156263A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037
CURRENT APPLICATION NUMBER: 0S/09/974,298
CURRENT APPLICATION NUMBER: 60/238,331
FRIOR FILING DATE: 2001-10-04
FRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SEQ ID NO 144
LENGTH: 2641
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US-09-974-298-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1063; Conservative
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Best Local Similarity
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LOCATION: 2635
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US-09-974-298-144
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                                                                                                                                                   APPLICANT: Jiradej Manosroi
APPLICANT: Chacchai Tayapiwatana
APPLICANT: Chacchai Tayapiwatana
APPLICANT: Friederich Goetz
APPLICANT: Friederich Goetz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tpA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT APPLICATION NUMBER: 2001-11-14
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-02-15
PRIOR PLING DATE: 2001-02-15
PRIOR PLING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches
                                                           Sequence 5, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION
APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-987-455-5
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OTHER INFORMATION: 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)
Page

-___CANT: NGUYEN, CATHERINE

APPLICANT: VIENS, PATRICE

APPLICANT: VIENS, PATRICE

APPLICANT: FERT, VINCENT

TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

TITLE OF INVENTION: GAING ARRAYS OF CANDIDATE GENES

FILE REFERENCE: 1546-R-00

CURRENT APPLICATION NUMBER: US/10/007,926A

CURRENT FILING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 468

SOFTWARE: PALENTIN VET. 2.1

SEQ ID NO 433

LENGTH: 329
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Patent No. US20020131964A1

GENERAL INFORMATION:

APPLICANT: CINES, Douglas B

APPLICANT: HIGAZ, Abd Al-Roof

TITLE OF INVENTION: TISSUE CONTRACTABILITY

FILE REFERENCE: 9596-331

CURRENT APPLICANTON NUMBER: US/09/880,503

CURRENT FILING DATE: 2001-06-13
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Pred. No. 4.3e-63;
0; Mismatches 6; Indels 0;
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; OTHER INFORMATION: a, t, c or
US-10-007-926A-433
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Best Local Similarity 97.5%;
Matches 232; Conservative
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OTHER INFORMATION: a, t, c
FEATURE:
NAME/KEY: modified base
LOCATION: (159)
OTHER INFORMATION: a, t, c
FEATURE:
NAME/KEY: modified base
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OTHER INFORMATION: a, t,
FEATURE:
NAME/KEY: modified_base
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NAME/KEY: modified_base
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ORGANISM: Homo sapiens
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US-09-880-503-15
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APPLICANT: BERTUCCI, FRANCOIS; APPLICANT: HOULGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
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US-10-007-926A-433
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Stelmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITION:
TITLE OF INVENTION: THERRY OF BREAST CANCES;
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/199,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14004
SOFTWARE: FREEEEQ for Windows Version 4.0
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US-09-735-705-122
Sequence 122, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
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| LOCATION: 1, 2, 3, 1414, 1415

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US-10-198-846-12748
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Matches 249; Conservative
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ORGANISM: Homo sapiens
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US-10-198-846-12748
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                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                              Score 191.6; DB 10; Length
Pred. No. 1.5e-50;
0; Mismatches 459; Indels
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  60/212,847
                                                                                                                                                                                                                                                              18.0%;
52.3%;
                     PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 1212
PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                            Query Match 18.0
Best Local Similarity 52.3
Matches 549; Conservative
                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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GACTGGAATTGTGAGCTGGGGCCGTGGATGTGCCCTGAAGGACAAGCCAAGCGTCTACAC
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1226 TICCCTCCAAGGCCGCATGACTTTGACTGGAATTGTGGGCTGGGGCCGTGGATGTGCCCT 1285
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                                                                                                                             1004 GTTTGGCACAAGCTGTGAGATCACTGGCFTTTGGAAAAGAGAATTCTACCGACTATCTCTA 1063
                                                                                                                                                                                                                   1064 TCCGGAGCAGCTGAAGATGACTGTTGTGAAGCTGATTTCCCACCGGGAGTGTCAGCAGCC 1123
                                         944 TGCGCAGCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGATCCCCA 1003
                                                                                                                                                                         813 ACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGG 872
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    633 TGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCC 692
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                                                                                        GGACTGGACGGACGGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCTTTCTA
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Patent No. US20020115139A1

GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
ITLE OF INVENTION: UNMBER: US/09/850,716A

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FREESEQ for Windows Version 3.0

SEG ID NO 122
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16.0%; Score 170.8; DB 10;
Best Local Similarity 51.3%; Pred. No. 7e-44;
Matches 551; Conservative 0; Mismatches 457;
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; ORGANISM: Homo sapien
US-09-850-716A-122
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US-09-850-716A-122
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Pred. No. 7e-44;
0; Mismatches 457; Indels
                                                                                                                                                                                                                                                         METHODS FOR
LUNG CANCER
                                                                                                                                                                                                        APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C;
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 122
Wang, Tongtong
Fan, Lidgun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                         Henderson, Robert A. McNeill, Patricia D.
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Best Local Similarity 51.3%;
Matches 551; Conservative (
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; ORGANISM: Homo sapien
US-09-735-705-122
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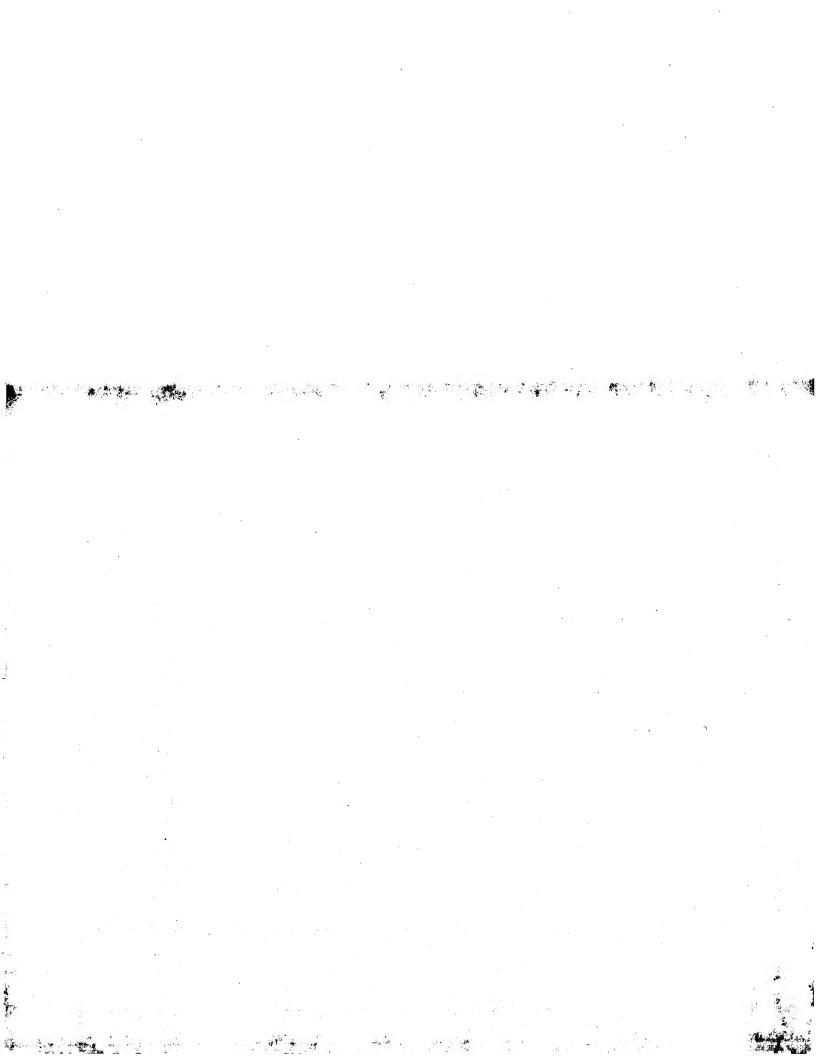
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CURRENT FILING DATE: 2001-06-28
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Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
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Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Henderson, Robert A.
Peckham, David W.
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Pred. No. 7e-44;
0; Mismatches. 457; Indels
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C4
CURRENT APPLICATION NUMBER: US/09/466,396A
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 122
LENGTH: 1475
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Sequence 122, Application US/09466396A
Publication No. US20030119763A1
GENERAL INFORMATION
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Best Local Similarity 51.3%;
Matches 551; Conservative
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US-09-466-396A-122
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BX329047 BX329047
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BX389609 BX389609
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13 BQ278177 13 BQ690978 13 BX389608 13 BX389608 13 BX389608 10 BE616613 12 BJ765247 13 BQ15720 14 BE616613 15 BG616613 16 BE732704 10 BE732704 11 BG68779 10 BE732704 11 BG68779 12 BM56995 13 BQ68779 14 BQ68779 15 BM569779 16 BW732101 18 BQ68779 19 AU134460 10 BE54949 11 BQ68794 11 BQ120780 10 BE54949 11 BE54949 10 BE54949 11 BU17993 11 BU17993 11 BU17993 12 BU17993 13 BU15721 14 CB12885 14 CB12885 14 CB12895 16 BW6927 17 BU190904 18 BU190904 11 BU190904 11 BU190904	1- PRI
115.8 76.6 993 1007.6 75.8 993	BX329047 BX329047 Homo sapien clone CSODI039XK15 3 BX329047.1 GI:30307 BX329047.1 GI:30307 BX7 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Mamalai, Butheria; Mull-length cDNA lib, Full-length cDNA conpertuc Library was construct Library
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 BX329047/C LOCUS DEFINITION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLLE JOURNAL COMMENT

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Directionally cloned using the following adaptors:
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5.-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                        AGENCOURT 8137213 Lupski dorsal root ganglion Homo sapiens cDNA Clone IMAGE:6184119 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Profurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
http://image.llnl.gov
Plate: LiAM13572 row: m column: 16
High quality sequence start: 18
High quality sequence stop: 644.
148 AGACTGTACCCATCCAGCCGCTGCACACACATTTACTTAACAGAACAGTCACCGAC
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                        Locacianism="Homo sapiens"

1. 930

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/clone="Ibe Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="Ist strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

268 c 282 g 194 t 2 others
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llarity 98.6%; Pred. No. 5.7e-223;
Conservative 0; Mismatches 12;
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Li, W. Tull-Unpub Conta Conta Conta Conta BP 19 Email Was n	/Organisme="rano" saplens" //wol type="mRNA" /db_xref="caxon:9606" /clone="CSODIO39YK15" /clone_Tib="Homo saplens PLACENTA COT 25-NORMALIZED" /clone_Tib="Homo saplens PLACENTA COT 25-NORMALI/ /note="lst strand cDNA was primed with a NorI-ob primer. Five prime end enriched, double-strand closested with Not I and cloned into the Not I are sites of the pCMVSPORT 6 vector. Library was not 203 a 290 c 277 g 191 t 1 others  79.9%; Score 850.6; DB 13; Length 962; imilarity 96.4%; Pred. No. 2.38-211;	191; Conservative 0; Mismatches 30; Indels 3; Gaps 192 GCCAGGCCATGGGCAAACTAATTACTGCCGGAATCCTGATGGGGATGCCAAG 1 GCCCAGGCACTGGGCAAACTAATTACTGCCGGAATCCTGATGGGGATGCCAAG 202 CCCTGGTGCCACGTGCTGAGAAACTGGCGGGGGTACTGTGTGGCCCTCC 2	TTCGCCGACATCGCCCCCCGGCAGCTGCCATCTTTGCCAAGCACAGAGGTCG CCCGGAGAGCGCTCCTGGCAGGCTGCCATCTTTGCCAAGCACAGAGGTCG CCCGGAGAGAGGTTCTCTGGCAGGGCATCTCTTGCCAGCTGCTCTCTGCC CCCGGAGAGGGGTTTCCGCCCCACCTGACGGTTTCTTGGGATTCTCTCTGCC GCCCACTGCTTCCAGAGAGGTTTCCGCCCCACCTGACGGTGATCTTGGGCAGAACA IIIIIIIIIIIIIIIIIIIIIIIIIIIII	AGGAATTCGATGATGACATTACGACAATGACATTGCGCTGCTGCTGCAAATCGGAT TCGTCCCGCTGTGCCTTACGACAATGACATTGCGCTGCTGCTGCAGAATCGGAT TCGTCCCGCTGTGCCCAGGAGAGAGCGGGGTCCGCACTGTGTGCCTTCCCCCGGCGGAC TCGTCCCGCTGTGCCCAGGAGAGCAGGGTCCGCACTGTGTGCCTTCCCCCGGCGGAC TCGTCCCGCTGTGCCCAGGAGAGCAGGGTCCTCCGCCTTGTGTGCCTTCCCCCGGCGGAC CTGCAGCTGCCGGACTGGACGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTG TCGTCCAGCTGCCGGACTGGACGAGTGTGAGCTCTCCGGCTACGGCAACCATGAGGCCTTG TCGTCCAGCTGCCGGACTGGACGGAGTGTGAGCCTTCCGGCTACGGCAACCATGAGGCCTTCCCCGGCTACGGCCAACCATGAGGCCTTCC
AUTHORS TITLE JOURNAL COMMENT FEATURES SOULC	BASE COUNT ORIGIN Query Match Best Local S	Matches Oy	6 8 8 8 8 8 8 8	2 4 5 4 5 4
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BQ278177 993 bp mRNA linear EST 07-MAY-2002
AGENCOURT_7061709 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5805153
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Pred. No. 5.2e-203;
0; Mismatches 14;
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111-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissum_type="dorsal root ganglia"
/dev stage="adult, 36 yr"
/lab_host="BH10B"
/clone=lib="Lupski dorsal root ganglion"
/note="Vector: pGWV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13576 row: m column: 22
High quality sequence stop: 665.
                                                                                                   CCCCTGGTGTGTGTGTGGGGGGGTGGGGTGGGGGGATCATCAGCCTGGGCCTG
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                                    601 TCTCCTTTCTATTCGGAGCGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCGC
                                                                                TGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGAC
                                                                                                                                                  ACTOGGAGOGGCGGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGC
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/db_xref="taxon:9606"
/clone="IMAGE:6185661"
                                                                                                                                                                                                                                                                                                                                                      1042 ATTCGTGACAACATGCGACCGTGA 1065
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AUTHORS
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BQ690978

AGENCOURT B046707 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6209120 5', mRNA Sequence.
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     360 CATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCCAGGAGAGCAGCGTGGT 419
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: Robert Strausberg, Ph.D.
Email: gapber = r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM2367 row: o column: 09
High quality sequence stop: 658:
                                                                                   660 CGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGAC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 110"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6209120"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:805153"
/tissue type="teratocarcinoma, cell line"
/tissue type="teratocarcinoma"
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                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 993)
NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution information
Clone through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2043 row: o column: 10
High quality sequence stop: 681.
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76.6%; Score 815.8;
Best Local Similarity 99.6%; Pred. No. 2.9e
Matches 828; Conservative 0; Mismatches
5', mRNA sequence.
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BQ278177.1 GI:20488385
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Vertebrata; Euteleostomi;

Craniata, Vertebrata, Eutele Catarrhini, Hominidae, Homo.

Eukaryota, Metazoa, Chordata, Craniata, Verte Mammalia, Eutheria, Primates, Catarrhini, Hor 1 (bases 1 to 918) Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Unill-length cDNA libraries and normalization Unpublished

sapiens (human)

Homo

Homo sapiens

Contact: Genoscope Genoscope Genoscope - Centrer National de Sequencage BP 191 91006 BVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr days normalized .lbrary was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4998.r For more information about this cluster, see

http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSOBAF025ZG09 AF02376\_2&cluster=4498.r. contact. Feng Liang Email : fliang@llfetech.com URL http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOBAF025ZG09\_AF02376\_2. Location/Qualifiers

/organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606"

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/close="Csday: 25" / close="Csday: 25" / close="Csday: 25" / close="Csday: 25" / close="Csday: 25" / close="Dia="PLACENTA COT 25-NORMALIZED" / close="lib="Home sapiens PlaceNTA COT 25-NORMALIZED" / note="list strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and closed into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.

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                                                                                                                                                            GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGGGCCTGAGACAGTACA
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                                                                                        ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCA
                                                                                                                                      230 GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGGCCTGAGACAGTACA
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                                                                                                                                                                                                            GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA
                                       Gaps
                                   3,
Score 807.6; DB 13; Length 918;
Pred. No. 4e-200;
0; Mismatches 29; Indels 3;
                                                                     ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGC
 75.8%;
                                   Matches 855; Conservative
                   Similarity
                                                                     170
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BX389608

BX389608 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI039YK15 5-PRIME, mRNA sequence.

BX389608.1 GI:30463469

DEFINITION ACCESSION VERSION

BX389608 LOCUS

9

120

293

Gaps

413

180 473 240

300

533

360

653 420 713

593

480

773 540 833 900 893 9 953 720

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954 TTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCC-GGGTGTGT 1012
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                                                                                                                                      GACGIGGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCA
                                                                                                                                                                                       GCCTCAGITICGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGC
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                                                                                                                                                                                                                                                                                                                                     CATCAGCTCCTGCTGGATTCTCTCTGCCGCCCCACTGCTTCCAGGAGGATTTCCGCCCCA
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                                                                               5,
                                           DB 13; Length 930;
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                                                                               Indels
                                                                               3,
                                       Score 796.2; DB 13
Pred. No. 3.8e-197;
0; Mismatches 3;
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                                           74.8%;
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                                         Query Match 74.8
Best Local Similarity 99.4
Matches 820; Conservative
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH1 MGC_109;
/clone_lib="NH1 MGC_109;
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoR1; Site_2:
Xho1; cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/Kho1 sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                      1001
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LinL at:
found through the I.M.A.G.E. Consortium/LinL at:
http://image.lnl.gov
Plate: LLCM2780 row: g column: 13
High quality sequence stop: 639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                               CAGTCACCGANCACATGCTGTGTGTGCTGGAGACACTCGNAGCGGCGGNCCCCA-GCAAACT
617 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACCATCACATTTACTTAACANGA
                                                                                                                                                                                                                                                                                               557 AGCICICCGGCIACGGCAAGCAIGAGGCCTIGICTCICITICIATICGGAGCGGCIGAAGG
                                                                                                                             AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTAACTAAAAA
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AGENCOURT 10412263 NIH_MGC 109 Homo sapiens cDNA clone IMAGE:6578533 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           1008 TGTGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACA 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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/db_xref="taxon:9606"
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AUTHORS
TITLE
JOURNAL
COMMENT
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AGENCOURT\_8043192 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6084476 BU157720

888 780 945

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BI765247 916 bp mRNA linear EST 25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 916)
                               GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCCCGCTGTGCCCAGGAGAGAGCCAGG
                                                                                          GTCCGCACTGTGTGCCTTTCCCCCGGCGGACCTGCAGCTGCCGGACTGAGACGGAGTGTGAG
                                                                                                                GTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGGAGGTGTGAG
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                                                                                                                                                                                                        GCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACA
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      GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11476 row: k column: 09
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/db_xref="taxon:966"
/clone="taxon:966"
/lab_host="mydE:29656"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 837.
Location/Qualifiers
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/clone=InAGE:608476"
/tissue type="ductal carcinoma, cell line"
/lab_host="bull ghage-resistant)"
/clone lib="NHH MGC l10"
/clone lib ling home lib laboratory of Garald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH—MGC Library."
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                                                          NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2316 row: e column: 21
High quality sequence stop: 630.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2550 row: p column: 02
High quality sequence start: 35
High quality sequence stor: 884.
                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 4.9e-189;
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Homo sapiens (human)
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| vorganism="Homo sapiens" |
| vorganism="Homo sapiens" |
| vorganism="Homo sapiens" |
| volone="mRMAGE:3611007" |
| volone="INAGE:3611007" |
| volone="type="adenocarcinoma" |
| volone=1ib="NIH_MGC_39" |
| volone=1ip="NIH_MGC_39" |
| volone=1ib="NIH_MGC_39" |
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM267 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 759.
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                               GCTGTGCCCAGGAGCAGCGTGGGTCCGCACTGTGTGCCTTCCCCCGGGGGGACCTGCAGC
                                                                                                                         TGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTT
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/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="NUNE (phage-resistant)"
/lab_host="NUNH MGC 49"
/clone lib="NUNH MGC 49"
/clone lib="NUNH MGC 49"
/clone lib="Organ: skin, Vector: porB7; Site 1: XhoI; Site 2:
EcoR1; CDNA made by oligo-dr priming. Directionally cloned
into EcoR1/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
I: 8kb. Library constructed by Ling Hong in the laborarory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. || Library. 
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                                                                                                                                                                                                                                                                Context: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC/DTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyre Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1719 row: n column: 21
High quality sequence stop: 810.
Location/Qualifiers
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Pred. No. 2.6e-171;
0; Mismatches 36; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                      BG763582.1 GI:14074235
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 974)

S. NIH-WGC http://mgc.nci.nih.gov/.

L. Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2645 row a column: 06
High quality sequence stop: 603.
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Xhol; cDNA made by oligo-dT priming. Directionally clone into EccRI/Xhol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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601571366F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3925600 5', BE732704

RESULT 15 BE732704 LOCUS DEFINITION ACCESSION

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//db_xref="taxon:9606"
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM752 row: d column: 17
High quality sequence start: 3
High quality sequence stop: 701.
Location/Qualifiers
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1 (bases 1 to 709)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 99.7%; Pred. No. 2.5e-170;
Matches 705; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                    Homo sapiens (human)
                                                                              Homo sapiens
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Search completed: August 19, 2003, 08:29:17 Job time: 3116.64 secs

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August 18, 2003, 19:53:48; Search time 75.5794 Seconds (without alignments) 9743.047 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	30833 Sequ	1267	288	I09039 Sequence 2	≰		Sequenc	F	A27431 DNA sequenc	∢ 4	۸ ک	Se	Sequenc	AR059991 Sequence	òξ	F	F	E01942 Synthetic D	≥۶	Se	စ္တန	A27729 DNA sequenc	Se	Sequence	nthetic	Ношо вар	lA seque	AZ/43/ UNA Beguenc	Se	Sequenc	Sequenc	sequence	nthetic	nthetic	E01941 Synthetic D A30593 DNA for tis			1	linear PAT 28-JUN-2002				1081	ion in prokaryotes
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Goetz,F., Werner,R.G., Tayapiwatana,C., Manosroi,A. and Manosroi,J. Methods for large scale production of recombinant dna-derived tpa or k2s molecules
Patent: WO 0240650-A 22 23-MAY-2002;
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Patent: WO 8808878-A 2 17-NOV-1988;
Location/Qualifiers
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AX431288
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3 c 6 g 3 t
                         1..18
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/note="coding sequence of the N-terminal part of K2S
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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Sequence 1 from Patent WO0240650.
AX431267
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EU1943 1065 bp DNA linear PAT 29-SEP-1997
Synthetic DNA encoding new t-PA tissue plasminogen activator.
E01943
                                                                     Goetz,F., Werner,R.G., Tayapiwatana,C., Manosroi,A. and Manosroi,J. Methods for large scale production of recombinant dna-derived tpa or kSs molecules
Patent: WO 0240650-A 4 23-MAY-2002;
BOEHRINGER INGELHEIM INT (DE)
Location/Qualifiers
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Methods for large scale production of recombinant dna-derived tpa
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1 (Dases 1 to 1065)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J: and
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="coding sequence for K2S protein"
a 314 c 312 g 214 t
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
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Patent: WO 0240650-A 7 23-MAY-2002;
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Sequence 7 from Patent WO0240650.
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artificial sequences.
1 (Dases 1 to 105)
Niwa, M., Saito, Y., Sasaki, H., Hayashi, M., Notani, J. and
Nobayashi, M.
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Niwa,M., Saito,X..., Sasaki,H., Hayashi,M., Notani,J. and
Kobayashi,M.
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                                                                                  1065 bp DNA DNA sequence of coding region in pthTTtrp. A27447
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1 Similarity 100.0%; Pred. No. 1.1e+02;
18; Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
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314 c 311 g 215 t
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                                                                                                                                                                                                                                                                                        New tissue plasminogen activator
Patent: EP 0302456-A 47 08-PEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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Patent: (US 5840533-A KO 24-NOV-1998;
Location/Qualifiers
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AX431270
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314 c / 311 g
638 TCTGAGGGAAACAGTGAC 655
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Matches 18; Conservative
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Query Match

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artificial sequences.
1 (bases 1 to 1068)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and
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synthetic construct
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1 (bases in the sequences)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and
Kobayashi,M.
New tissue plasminogen activator
Patent: EP 0302456-A 39 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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DNA sequence of coding region in pTTiPAdeltatrp.
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315 c 312 g 216 t
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Patent: EP 0302456-A 33 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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Kobayashi, M.

NOVEL TISSUE PLASMINOGEN ACTIVATION FACTOR
Patent: JP 1989104167-A 10 21-APR-1989;
FUJISAWA PHARMACEUT CO LTD
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1989104167-A/10
PD 21-APR-1989
PP 01-AuG-1987 GB 87 8718298, 26-OCT-1987 GB 87 8725052, PR
PR 01-AuG-1987 GB 87 8718298, 26-OCT-1987 GB 87 8726683
PR 01-AuG-1987 GB 87 8726683
PR CARANASHI MASAKAZU
PC CL2N9/64,C12R1:91);
CC CL2N9/64,C12R1:91);
CC STAND6068SS: Double;
CC STAND6068SS: Double;
CC Argothetical: No;
CC Topology: Linear;

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Niwa, M., Saito, Y., Sasaki, H., Hayashi, M., Notani, J. and
Kobayashi, M.
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100.0%; Pred. No. 1.1e+02;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
db_xref="taxon:32630"
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Patent: EP 0302456-A 31 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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E 1 (bases 1 to 1068)

Kobaysshi,M.
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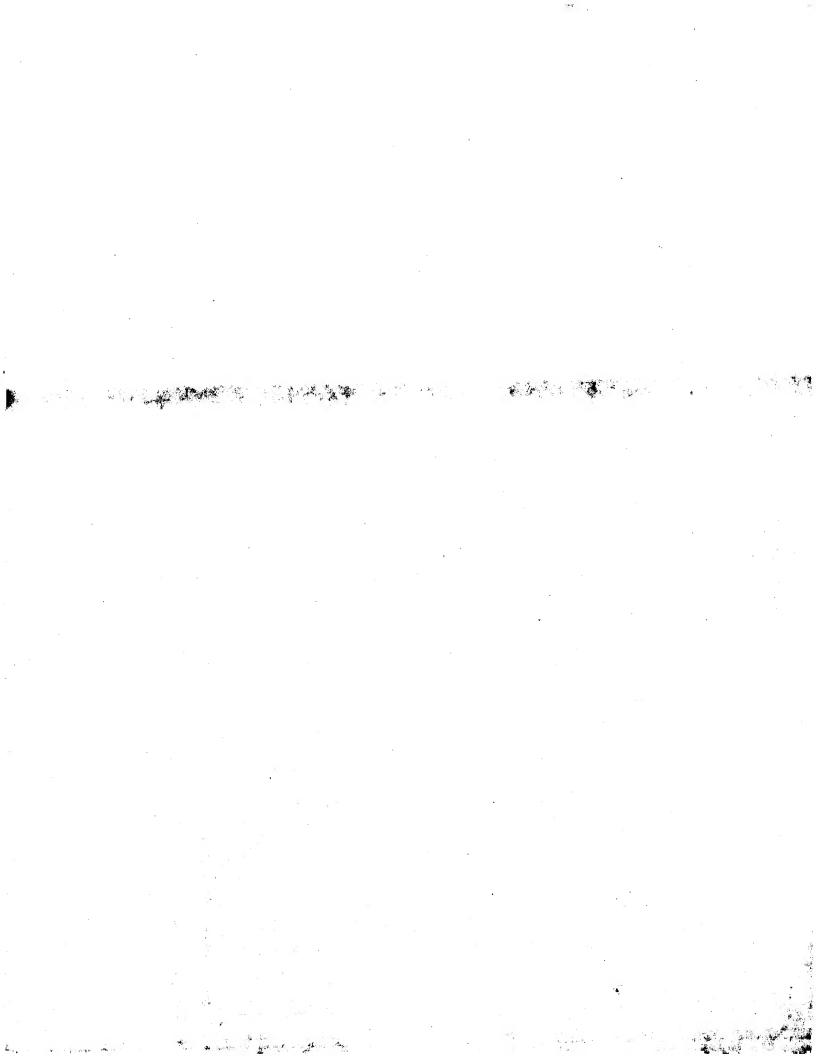
Tissue plasminogen activator

Tissue plasminogen activator
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Niwa, M., Saito, Y., Sasaki, H., Hayashi, M., Notani, J. and
Kobayashi, M.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Patent: EP 0302456-A 45 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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## ALIGNMENTS

WPI; 2002-471625/50.

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ecreted, active, correctly folded, recombinant tissue plasminogen activator (tPA), Kringle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vain thrombosis or related diseases associated with unwanted blood clotting. The present sequence
                                                                                                                        Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
                                                                                                                                                                                                                                       present invention relates to a method of producing extracellularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human K2S heterologous protein N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA-derived heterologous protein; OmpA; K2S; kringle 2; serine protease; human; ds.
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                                              Manosroi J, Manosroi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tayapiwatana C, Manosroi J, Manosroi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 18; DB 24; Length 18; 100.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human K2S heterologous protein N-terminal peptide DNA #2
                                                                                                                                                                                                                                                                                                                                                                                                                              is a DNA fragment encoding OmpA N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 6 A; 3 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
              (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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                                              Tayapiwatana C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                     2; Page 29; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGAGGGAAACAGTGAC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD38989 standard; DNA; 18 BP.
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/*tag= a
/product= "H
peptide #2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
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                                              Goetz F,
                                                                          WPI; 2002-519376/55.
P-PSDB; AAE25033.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200240696-A2
                                                                                                                                                                         peptide OmpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                              Werner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD38989;
                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                      The
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                                                                                                                                                                               heterologous protein in prokaryotic cells, where the heterologous protein is secreted extracellularly as an active and correctly folded protein and
                                                                                                                                                                                                             the prokaryotic cell contains and expresses a vector comprising the DNA coding for the heterologous protein operably linked to the DNA coding for the signal peptide OmpA or its functional derivative. The method is useful for commercial large-scale production of heterologous proteins, e.g. K2S (kringle 2 plus serine protease), in prokaryotic cells, and is generally applicable in the expression of several different proteins and polypeptides which do not require mammalian glycosylation in prokaryotic host cells. The method may also be used to obtain DNA sequences of a protein of interest to be expressed from databases and cloned for use. The present sequence is human K2S heterologous protein N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT15487-T15498 are PCR primers used for the isolation and amplification of cDNA encoding a human megakaryocyte differentiation/proliferation factor, NTPO, some of the primers may also be used to engineer
                                                                                                                                                            The invention relates to a method for producing recombinant DNA-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Megakaryocyte differentiation/proliferation factor, NTPO cDNA primer.
                                 Producing recombinant DNA-derived kringle 2 plus serine protease, comprises using a prokaryotic cell expressing a vector having a DNA coding for a heterologous protein operably linked to a DNA coding fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Megakaryocyte differentiation/proliferation factor - and fragments of it are prepared by recombinant techniques and used for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Megakaryocyte; differentiation factor; proliferation; recombinant; thrombocytopenia; NTPO; polymerase chain reaction; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 6 A; 3 C; 6 G; 3 T; 0 other;
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                                                                                                                           Disclosure, Page 22, 52pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 18; Conservative
                                                                                         the signal peptide OmpA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-117001/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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Indels

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Mismatches

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18; Conservative

Matches

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ZS; cardiac infearction; acute myocardial infarction; pulmonary embolism; 
artery occlusion; deep vein thrombosis; blood clotting; thrombolytic; 
cerebroprotective; cardiant; PCR; primer; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method of producing extracellularly accived, active, correctly folded, recombinant tissue plasminogen activator (tPA), kringle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vain thrombosis or related diseases associated with unwanted blood clotting. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
recombinant NTPO DNA. DNA encoding the factor can be used to produce a recombinant NTPO at a high yield. NTPO is useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases associated with unwanted blood clotting. The present sequence is a PCR primer which is used for amplifying human tissue plasminogen activator (tPA) gene. This primer is used in the exemplification of
                                                                                                                                                              Gaps
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                                                                                                                   100.0%; Score 18; DB 17; Length 42; 100.0%; Pred. No. 11; 1. Indels ive 0; Mismatches 0; Indels
                                                                               Sequence 42 BP; 10 A; 9 C; 11 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tPA gene amplifying PCR primer, sK2/174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tayapiwatana C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 80; 80pp; English.
                                                                                                                                                                                                  1 TCTGAGGGAAACAGTGAC 18
                                                                                                                                                                                                                           31 TCTGAGGGAACAGTGAC 14
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                                                                                                                                                                                                                                                                                                                                    AAD40621 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                     Local Similarity 100.
les 18; Conservative
                                        of thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-519376/55.
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Matches
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Score 18; DB 24; Length 42; Pred, No. 11;

100.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                    Human tissue plasminogen activator (tPA) gene amplifying primer, sK2/174.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is human tissue plasminogen activator (tPA) gene amplifying PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing recombinant DNA-derived kringle 2 plus serine protease, comprises using a prokaryotic cell expressing a vector having a DNA coding for a heterologous protein operably linked to a DNA coding ftee signal peptide OmpA.
                                                                                                                                                                                                                                                                                  Recombinant DNA-derived heterologous protein, OmpA; K2S; kringle 2; serine protease; human; primer; PCR; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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                                                                                                                                                В.
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                               1 TCTGAGGGAAACAGTGAC
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AAT16011/c
ID AAT16011 standard; DNA; 55
XX
                                                                                                                                               AAD38990 standard; DNA; 42
                                                                                                                                                                                                                   23-SEP-2002 (first entry)
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hes 18; Conservative
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                                                                                                                                                                                  AAD38990;
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Matches
                                                                                                                 RESULT 5
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23-SEP-1996

AAT16011;

WO9603434-A1

Synthetic.

25-JUL-1995; 25-JUL-1994;

08-FEB-1996.

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Blood, tissue plasminogen activator; tPA, mutein; stability; tPA-1; physiological; activity; tPA-2; pTB 1127; mutagenesis; plasmid; truncated; deletion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bovine papilloma virus DNA and used to transfect C127 mouse cells.
/*tag= c
/label=synthetic oligomer
/note="capable of being transcribed into an mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant sequence was obtained upon ligation of a 184bp Ddel-EcoRI fragment of p7BDT-10, a 730bp Sall EcoRI fragment of p7BDT-10, a 730bp Sall EcoRI fragment of p7BDT-10 encoding N-terminal portion of t-PA and a synthetic oligomer capable of being transcribed into an mRNA stop codon. The ligated product was cleaved with Sall to give the 952bp fragment shown. This fragment was cloned into the XhoI site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 18; DB 9; Length 952; 100.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                  DNA coding for tissue plasminogen activator A chain -
used as labelled A chain for antithrombotic drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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/note= "Position of deletion mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                        stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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                                                                                                                                                                                                    87US-0050950.
88WO-US01624.
                                                                                                                                                                  88WO-US01624
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                                                                                                                                                                                                                                                         (INTE-) INTEG GENETICS INC.
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nes 18; Conservative
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                                                                                                                                                                  12-MAY-1988;
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12-MAY-1988;
                                                                                          WO8808878-A
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                                                                                                                              17-NOV-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tPA-2 cDNA
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                                                                                                                                                                                                                                                                                           Reddy VB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATIGO11-T16014 are PCR primers used for the isolation and amplification of the human tissue-plasminogen activator (t-PA) gene. The T-PA gene may be incorporated into a plasmid contg. DNA encoding a megakaryocyte differentiation/proliferation factor, NTPO, so as expression produces a chimeric t-PA-NTPO protein. DNA encoding the factor can be used to produce a recombinant NTPO at a high yield. NTPO is useful for the treatment of thrombocytopenia either alone or in conjunction with
                                                                    Human tissue-plasminogen activator (t-PA) gene N-terminal PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Megakaryocyte differentiation/proliferation factor - and fragments of it are prepared by recombinant techniques and used for treatment of thrombocytopenia
                                                                                                       Megakaryocyte, differentiation factor; proliferation, recombinant;
thrombocytopenia; NTPO; polymerase chain reaction; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant human tissue plasminogen activator A chain sequence.
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antithrombotic agents; ds.
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/product=t-PA A-chain
915..952
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14..118
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                                                                                                                                                                                                                                                                                                                                                                                  Yoshitake S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN80896 standard; cDNA; 952 BP
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119..943
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Matches 18; Conserv
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Homo sapiens

sig\_peptide mat\_peptide

31-OCT-1990

AAN80896;

AAN80896

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Query Match

misc\_feature

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Gaps

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Tissue plasminogen activator; tPA; kringle 2 serine protease; stroke; KZS; carddac infarction; pulmonary embolism; artery occlusion; deep vein thrombosis; blood clotting; thrombolytic; cerebroprotective; cardiant; ompA; enzyme; human; gene; ds.
              The sequences given in AAQ40663-64 are cDNAs encoding tissue plasminogen activator (LPA) muteins, LPA-7 and LPA-8. These muteins are truncated versions of LPA (see AAQ40654). LPA-7 further comprises a Glu-Argy-Tyr-His muteation amino acide corresponding to amino acide 303-304 of LPA and tPA-8 further contains a deletion of amino acide sorresponding to amino acide 296-302 of tPA, and the mutation contained in tPA-7. The plasmid pTB 1277 was treated with the synthetic oligomers given in AAQ40661-62 in an in vitro mutagenesis system. The tPA muteins, tPA-7 and -8 have good stability in blood and good physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted, active, correctly folded, recombinant tissue plasminogen activator (FPA), Kringle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method of producing extracellularly
                                                                                                                                                                                                             100.0%; Score 18; DB 14; Length 1047; 100.0%; Pred. No. 16; 0; Indels 0;
                                                                                                                                                                                  Sequence 1047 BP; 221 A; 308 C; 301 G; 217 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tayapiwatana C, Manosroi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Human K2S protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human kringle 2 serine protease (K2S) DNA.
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1..1065
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                                                                                                                                                                                                                                                                             1 TCTGAGGGAACAGTGAC 18
                                                                                                                                                                                                                                                                                              4 TCTGAGGGAAACAGTGAC 21
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAD40616;
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                                                                                                                                                        activity
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                                                                                                                                                                                  The sequences given in AAQ40657-58 are cDNAs encoding tissue plasminogen
                                                                                                                                                                                               activator (tPA) muteins, TPA-1 and tPA-2. These muteins are truncated versions of tPA (see AAQ40654) and tPA-2 further contains a deletion of amino acids corresponding to amino acids 296-302 of tPA. The plasmid pTB 1127 was treated with the synthetic oligomers given in AAQ40655-56 in an in vitro mutagenesis system. The tPA muteins, tPA-1 and -2 have good stability in blood and good physiological activity.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blood; tissue plasminogen activator; tPA; mutein; stability; tPA-7; physiological; activity; tPA-8; pTB 1277; mutagenesis; plasmid; truncated; deletion; mutation; ss.
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                                                                                                                                                                                                                                                                                                                                    Score 18; DB 14; Length 1047; Pred. No. 16;
                                                                                                        for treating
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/note= "Position of deletion mutation"
                                                                                                                                                                                                                                                                                                        Sequence 1047 BP; 220 A; 307 C; 305 G; 215 T; 0 other;
                                                                                                        Tissue plasminogen activator mutein - useful f myocardial infarction and cerebral thrombosis
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                    Disclosure; Page 26-27; 92pp; Japanese.
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371..376
/*tag= b
/note= "GAGCGG>TATCAC"
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                            (TAKE ) TAKEDA CHEM IND LTD
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                          P-PSDB; AAR35401
 25-DEC-1990;
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25-DEC-1990;
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Manosroi A;

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Synthetic.
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       for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vein thrombosis or related diseases associated with unwanted blood clotting. The present sequence is human X2S DNA.
                                                                                                                      Gaps
Sequences of the invention are useful for manufacturing a medicament
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                                                                                                100.0%; Score 18; DB 24; Length 1065; 100.0%; Pred. No. 17; 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising finger and growth factor domains lacking tPA for longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                                                                                                              Tissue plasminogen activator; tPA; thrombolytic agent; plasminogen; vascular diseases.
                                                                             Sequence 1065 BP; 225 A; 314 C; 312 G; 214 T; 0 other;
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                                                                                                                                                                                                                                                                                          Sequence of coding region in plasmid puTTtrp
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                            AAN91128 standard; DNA; 1066 BP
                                                                                                                                        1 TCTGAGGGAAACAGTGAC 18
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87GB-0025052.
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Best Local Similarity 100.0%
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Best Local Similarity 100.
Matches 18; Conservative
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26-OCT-1987;
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Gaps
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                                                                                                                                                                                                                                                                                                                 Tissue plasminogen activator; tPA; thrombolytic agent; plasminogen; vascular diseases.
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                                                                                                                                                                                                                                                                            Sequence of coding region in plasmid pST112.
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4 rcreaeceaaceacicae 21
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87GB-0025052.
87GB-0026683.
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P-PSDB; AAP94407.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1987;
26-OCT-1987;
13-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
03-OCT-2002
18-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-1988;
                                                                                                                                                                                                                                18-JUN-1990
                                                                                                                                                                                       25-MAR-2003
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Gaps

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0; Indels

0; Mismatches

1 TCTGAGGGAAACAGTGAC 18

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Hybrid monoclonal antibody - used for prepn. of thrombolytic drug having increased thrombolytic activity and specificity and reduced reactivity to fibrinogen
                                                                                                           Saito Y, Sasaki H, Hayashi M, Notani J, Kobayashi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..1068
/*tags a
/product= tPA-1
/note= "encodes Kringle-2 and protease domains"
                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 18; DB 10; Length 1068; Best Local Similarity 100.0%; Pred. No. 17; Matches 18; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis targetted antithrombotic agent; hybridisation probe; Kringle domain; protease; ds.
                                                                                                                                                                                                  New tissue plasminogen activator - comprising finger and growth factor domains lacking tPA for longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1068 BP; 228 A; 313 C; 312 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                            (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human truncated tPA-1 mutein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ53320 standard; cDNA to mRNA; 1068 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                            Disclosure; Page ?; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 7; 38pp; Japanese
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   87GB-0018298.
87GB-0025052.
87GB-0026683.
                                                                       (FUJI ) FUJISAWA PHARM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1994 (first entry)
                                                                                                                                               WPI; 1989-040625/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-408334/51.
P-PSDB; AAR44836.
                                                                                                                                                                    P-PSDB; AAP94411.
 03-AUG-1987;
26-OCT-1987;
13-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP05304992-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ53320;
                                                                                                             Niwa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 18; DB 10; Length 1068; Best Local Similarity 100.0%; Pred. No. 17; Matches 18; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising finger and growth factor domains lacking tPA for longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; tPA; thrombolytic agent; plasminogen; vascular diseases.
Tissue plasminogen activator; tPA; thrombolytic agent; plasminogen; vascular diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1068 BP; 225 A; 315 C; 312 G; 216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                  Saito Y, Sasaki H, Hayashi M, Notani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of coding region in plasmid pSTTktrp.
                                                                                       Location/Qualifiers
1..1065
/*tag= a
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1..1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tissue plasminogen activator -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page ?; 68pp; English.
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87GB-0025052.
87GB-0026683.
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(updated)
(first entry)
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P-PSDB; AAP94408.
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26-OCT-1987;
13-NOV-1987;
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03-OCT-2002
18-JUN-1990
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                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                  Niwa M,
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Gaps

XX
CC Site-directed mutagenesis was carried out on a human tPA cDNA
CC template. The resulting mutated coding sequence encoded a Met
CC residue followed by amino acids 174-527 (i.e. the Kringle 2
CC and protease domains) of mature wild-type tPA. The mutein has
CC increased thrombolytic activity and very little reactivity to
CC fibrinogen. Monoclonal antibodies specific for fibrin are used in
CC the production of bispecific monoclonal antibodies which also
CC recognise truncated tPA muteins such as tPA-1 lacking the finger,
CC EGF and Kringle 1 domains.
XX
Sequence 1068 BP; 226 A; 314 C; 313 G; 215 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 1068; Best Local Similarity 100.0%; Pred. No. 17; Matches 18; Conservative 0; Mismatches 0; Indels 0; Qy I TCTGAGGGAAACGTGAC 18

; 0

0; Gaps

Search completed: August 18, 2003, 23:28:45 Job time : 6.34127 secs

Db 4 TCTGAGGAAACAGTGAC 21

Seguence Seguence

Sequence 61, Appli Sequence 3, Appli Sequence 3, Appli Sequence 19, Appli Sequence 19, Appli Sequence 6, Appli Sequence 46, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 11, Appli Sequence 11, Appli

Sequence 977, A Sequence 3, App Sequence 51, Ap

Sequence

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Minimum DB Maximum DB

Database

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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HOTANI, JOUJI
APPLICANT: NOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STAFE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Plan PC Compatible
COMPUTER: Plan PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/88/811,949
FILING DATE: 05-MAR-1997
CLEASTFICATION NUMBER: 24.618
REFERENCE/DOCKET NUMBER: 24.618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEFAK: 703-413-3000
TELEFAK: 703-413-3000
TELEFAK: 703-413-3000
TELEFAK: 703-413-3000
SEQUENCE CHARACTERISTICS:
FOWATHOR FOR SEQ ID NO: 60:
US-09-439-313-174
US-09-352-616A-174
US-09-956-243-114
US-09-966-243-114
US-08-146-930-3
US-08-458-240-3
US-08-458-240-3
US-08-30-6691B-19
US-08-30-6691B-19
US-08-930-601-19
US-09-206-942-46
US-09-803-671B-3
US-09-620-312D-977
US-08-373-190-51
US-08-438-190A-51
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                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 60, Application US/08811949; Patent No. 5840533; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
     1459
1459
1459
3775
5159
5159
5159
35100
35100
3222
322
64467
1681
1681
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US-08-811-949-60
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Sequence 42, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 25, Appl
Patent No. 5344773
Patent No. 5344773
Sequence 1, Appli
Sequence 1, Appli
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Sequence 174, App
Sequence 174, App
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                                                                                                         August 18, 2003, 22:51:23; Search time 1.40873 Seconds (without alignments) 5639.757 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, 1
Sequence 50, 1
Sequence 54, 1
Sequence 56, 1
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Patent No. 520
Patent No. 520
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Sequence 6
Sequence 6
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-811-949-38
US-08-811-949-42
US-08-119-512-3
US-08-488-015B-3
US-08-488-015B-3
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US-08-811-949-52
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US-08-811-949-64
US-08-811-949-64
US-08-811-949-50
US-08-811-949-54
US-08-811-949-54
US-08-811-949-54
US-08-811-949-56
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US-09-030-607-174
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                        569978 segs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - nucleic search, using sw model
                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                           1 tctgagggaaacagtgac 18
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seq length: 200000000
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18
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Match 1
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Score

8

Result

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; NAME/KEY:
; LOCATION:
US-08-811-949-46
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                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             SEE: P.C. ...., CLEBLAND, MAIER & NEUS: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
                                                                                                                                                                                                                                        APPLICANT: NIWA, MINEO
APPLICANT: SALTO, YOSHIMASA
APPLICANT: SASAITO, YOSHIMASA
APPLICANT: ASSAIT, HINOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
 Pred. No. 2.9;
                     Mismatches
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100.0%; Pred. No. :
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTATION NUMBER: 24,618
REFERENCE DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                  Sequence 44, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1068 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 703-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..1065
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Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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US-08-811-949-46
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CITY: AR
STATE: V
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APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
CORRESPEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                        STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MR-1997
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 18-966-0
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3200
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
TYPE: nuclaic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HIYOSHI
APPLICANT: HYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 677
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 52, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DY
MEDING SYSTEM: PC-DOS/MS-DY
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Best Local Similarity 100.0
Matches 18; Conservative
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COMPUTER READABLE FORM:
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: APPLICANT ANDRESSE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY, ARLINGTON
CONTRESSED: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 18; DB 2; Length 1068; Best Local Similarity 100.0%; Pred. No. 2.9; Matches 18; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 18; DB 2; Length 1170;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels (
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F:
REGISTRATION NUMBER: 24,618
REFRENCE/POCKET NUMBER: 18-966-0
TELECOMMULCATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3000
INFORMATION FOR EGO ID NO: 64:
SEQUENCE CHRAACTERISTICS:
LENGTH: 1170 base pairs
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 5840533
GENERAL INFORMATION:
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                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
       INFORMATION FOR SEQ ID NO: 58:
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                            SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
                                                                         TYPE: nucleic acid STRANDEDNESS: double
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular
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, LOCATION:
US-08-811-949-58
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; LOCATION:
US-08-811-949-64
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APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBATASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STREET: VACOUNTY.
                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
UNRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: 0BLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REPRENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-220
                                                                                                           APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELEPHONE: 703-413-3000
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTGAGGGAAACAGTGAC 18
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Best Local Similarity 100.0
Matches 18; Conservative
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GENERAL INFORMATION:
APPLICANT: NIWA, 1
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; LOCATION: 1...1
US-08-811-949-52
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ZIP: 22202
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Sequence 50, Application US/08811949
| Patent No. 5840533
| GENERAL INPORMATION:
| APPLICANT: NIWA, MINEO |
| APPLICANT: SASAKI, HITOSHI |
| APPLICANT: ASAKI, HITOSHI |
| APPLICANT: HAYASHI, MASAKO |
| APPLICANT: HAYASHI, HITOSHI |
| APPLICANT: NOTANI, JOUJI |
| APPLICANT: KOBAYASHI, MASAKO |
| APPLICANT: MUNGER OF SEQUENCES |
| TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR |
| NUMBER OF SEQUENCES |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: P.C. |
| ADDRESSEE: P.C. |
| ADDRESSEE: P.C. |
| ALINGTON |
| CITY: ARLINGTON |
| CITY: ARLINGTON |
| ALINGTON |
| CITY: ALLINGTON |
| ALINGTON |
| ALINGTON |
| CITY: ALLINGTON |
| ALINGTON |
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APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES:
67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM. *...

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIPICATION: 435
ATORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 18-966-0
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3200
TELEPHONE: 703-413-2200
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 10v..
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION:
US-08-811-949-48
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAJAKI, HIYOSHI
APPLICANT: SASAKI, HIYOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SUSTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/811,949

FILING DATE: 05-MRR 1997

CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: OBLON, NORMAN F:

REFERENCE/DOCKET NUMBER: 18-966-0

TELEPHONE: 703-413-3200

TELEPHONE: 703-413-220

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 1170 base pairs

TYPE: NUCLEIC ACID NO. 66:

STRANDEDNESS: double

TOPPY: ACID NO. 66:

TYPE: NUCLEIC ACID NO. 66:

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100.0%; Pred. No. 2.9
tive 0; Mismatches
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Patent No. 5840533
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    Sequence 66, Application US/08811949
Patent No. 5840533
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SAITO, YOSHIMASA
SASAKI, HITOSHI
HAYASHI, MASAKO
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.0
Matches 18; Conservative
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US-08-811-949-66
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APPLICANT:
APPLICANT:
APPLICANT:
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STATE:
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GENERAL INCORMATION:
APPLICANT: SING, YOSHIMASA
APPLICANT: SASAKI, HITOSHIMASA
APPLICANT: SASAKI, HITOSHIMASA
APPLICANT: HAYASHI, MASAKO
APPLICANT: HOYBAII, MASAKAZU
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 18; DB 2; Length 1314; 100.0%; Pred. No. 2.9; cive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                Query Match 100.0%; Score 18; DB 2; Length 1314; Best Local Similarity 100.0%; Pred. No. 2.9; Matches 18; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949 FILING DATE: 05-WAR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56, Application US/08811949
Patent No. 5840533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                           TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                LENGTH: 1314 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                           1.1311
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                                      TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                         , NAME/KEY:
, LOCATION:
US-08-811-949-54
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US-08-811-949-56
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STATE: VALINGTON
STATE: VA
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ZUE: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: OBLOW, NORMAN F
REGISTRATION NUMBER: 14,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HOTANII, JOUJI
APPLICANT: NOTANII, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. Matches 18; Conservative 0; Mismatch
                                                                                                                                                                              24,618
24,618
278: 18-966-0
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Patent No. 5840533
                                                                                         FILING DATE: 05-WAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REPERRING/DOCKET NUMBER: 18-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 50.
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TCTGAGGGAAACAGTGAC 18
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LOCATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Jarrell Ph.D., Brenda H.
REGISTRATHON NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0079571-0040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 248 5000
TELEPHONE: 617 248 4000
INFORMATION FOR SEQ 1D NO: 10: SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES: 34

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/53,412

FILING DATE: 22-MAY-1987
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                100.0%;
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                         Conservative
                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
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CITY: Boston
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LENGTH: 1738
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COUNTRY:
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APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYSAKI, HITOSHI
APPLICANT: HAYSAKI, MASAKO
APPLICANT: MOTANI, JOUJUI
APPLICANT: KOBAYASHI, MASAKAZU
APPLICANT: KOBAYASHI, MASAKAZU
APPLICANT: KOBAYASHI, MASAKAZU
CORRESPONDENCE: 67
CORRESPONDENCE: 67
CORRESPONDENCE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ** APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA, ; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                               SEE: P.C.
: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INCRMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/ODCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
                                                                                                                  Sequence 62, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
250 TCTGAGGGAACAGTGAC 267
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INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1419 base pairs
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Best Local Similarity 100.
Matches 18; Conservative
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EDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-811-949-62
                                                                                                    US-08-811-949-62
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Sequence 10, Application US/08814412
Sequence 10, Application US/08814412
Sequence 10, Application US/08814412
Sequence 10, Application US/08814412
SEQUENCE 10, Introduce Introduc
                                                                                                                                                                                                                                                                      Length 1724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             520340-1
;Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
;PATRICK J.;PINGEL, KURT;YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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APPLICATION NUMBER: US/08/814,412 FILING DATE: US/08/814,412 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                      Score 18; DB 6;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
SEQ ID NO:5:
; LENGTH: 1724
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; INMEDIATE SOURCE:
; CLONE: amplified t-PA clone
US-08-814-412-10

Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 3;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGAGGGAAACAGTGAC 18

Db 696 TCTGAGGGAAACAGTGAC 713
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Search completed: August 19, 2003, 08:35:04 Job time : 4.40873 secs

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August 19, 2003, 04:46:44; Search time 5.07937 Seconds (without alignments) 7930.701 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US60ABWPUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60ABWBUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1504479 seqs, 1118970152 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                        US-09-987-455-1
                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                           Run on:
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Description	Sequence 5, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 22, Appl	Sequence 4, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 12748, A	Sequence 6, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 144, App	Sequence 237, App	Sequence 18405, A	Sequence 6540, Ap
ΙD	US-09-987-457-5	US-09-987-455-1	US-09-987-457-6	US-09-987-455-22	US-09-987-455-4	US-09-987-455-7	US-09-987-455-2	US-09-987-455-5	US-10-198-846-12748	US-09-969-271-6	US-10-193-656-7	US-09-969-271-5	US-09-974-298-144	US-09-878-574-237	US-09-864-761-18405	US-09-960-352-6540
DB	1	11	11	11	11	11	11	11	14	6	14	σ	10	70	σ	10
* Query Match Length DB	18	18	42	42	1065	1065	1128	1128	1415	1689	2509	2519	2641	139	292	352
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	85.6	85.6	85.6
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SUMMARIES

Semience 2988		de '7*6* aniende	Sequence 1647, Ap	Sequence 39133, A	Sequence 243054,				Sequence 166216,		Sequence 85099, A	Sequence 947, App	174, #	Sequence 174, App	174,	174,	Sequence 174, App	e 174	174	174	174	174,	Sequence 3, Appli	Sequence 1699, Ap	Sequence 175, App		Sequence 23, Appl	51, 7	Sequence 61, Appl	
115-09-983-965-2988	110 00 000 000 1000	02-09-903-903-4942	US-09-864-761-1647	US-10-027-632-39133	US-10-027-632-243054			US-10-027-632-166215	US-10-027-632-166216	SD	US-10-027-632-85099			US-09-780-669-174	US-09-030-606-174	US-09-822-827-174	US-09-115-453-174	US-09-232-880-174	US-09-895-793-174	US-09-895-814-174	US-10-012-896-174	US-10-010-940-174	US-09-888-615-3	US-09-917-800A-1699	US-10-205-194-175	US-10-027-632-266063	US-09-813-432-23	US-09-989-722-61	US-09-989-723-61	
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15.4		ř.	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	
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## ALIGNMENTS

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APPLICANT: Manosroi, Aranya
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE REPERENCE: 0652.2180001
CURRENT APPLICATION NUMBER: 00/09/987,457
CURRENT PILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-02-15
PRIOR PLICATION NUMBER: 60/268,573
PRIOR PLILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 5:
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: coding OTHER INFORMATION: sequence of the N-terminal part of K2S molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
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Sequence 5, Application US/09987457
Publication No. US20030013150A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-987-457-5
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RESULT

25 TCTGAGGGAAACAGTGAC 42

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APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Priedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: Mchods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.190001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT APPLICATION NUMBER: 601-61-11-14
FRIOR APPLICATION NUMBER: 602-68,574
FRIOR APPLICATION NUMBER: 600-027779.8
FRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Aradiya manostoi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz

TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.120001
CURRENT APPLICATION NUMBER: 050001
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60,268,574
PRIOR APPLICATION NUMBER: 68 0027779.8
PRIOR APPLICATION NUMBER: GB 0027779.8
PRIOR PRILING DATE: 2000-11-14
SROTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 1065
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Pred. No. 7.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 18; DB 11; Length 42; Best Local Similarity 100.0%; Pred. No. 7.2; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                Sequence 22, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
APPLICANT: Aranya Manosroi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCTGAGGGAAACAGTGAC 18
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Best Local Similarity
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APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Werner, ROIf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE REFERENCE: 0652.2180001
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                                                                                                                         APPLICANT: Usedel Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Getz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
TOURRENT APPLICATION NUMBER: US/09/987,455
PRIOR FILING DATE: 2001-01-14
PRIOR PLING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver: 2.1
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US-09-987-457-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 18; DB 11; Length 18; 100.0%; Pred. No. 7.1;
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CURRENT FILING DATE: 2001-111-14
FRIOR PELING DATE: 2001-02-15
FRIOR APPLICATION NUMBER: 60/268,573
FRIOR APPLICATION NUMBER: GB 00 27 782.2
FRIOR APPLICATION NUMBER: GB 00 27 782.2
FRIOR APPLICATION NUMBER: GB 00 27 782.2
FRIOR PELING DATE: 2000-11-14
FRIOR PELING DATE: 2000-11-14
SOOTWARE: PALENTIN Ver. 2.1
FRIOR DATE
FRIOR FRIOR FRIOR NOS: 18
SOO ID NOS 6
FRIOR FRIOR FRIOR NOS: 18
Sequence 1, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
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Publication No. US20030013150Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Conservative
                                                                                               APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosr
APPLICANT: Chatchai Tayap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 18
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Gaps

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APPLICANT: Aranya Manosroi
APPLICANT: Aranya Manosroi
APPLICANT: Chardei Manosroi
APPLICANT: Chardei Manosroi
APPLICANT: Chardei Tayapiwatana
APPLICANT: Chardia Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Morb-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
FILE REFERENCE: 0652.2190001
CURRENT FILING DATE: 2001-01-15
PRIOR PLILNG DATE: 2001-02-15
PRIOR PLILNG DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Mang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT PILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
                                                                                     Length 1128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 18; DB 11; Length 1128; 100.0%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: coding OTHER INFORMATION: sequence for OmpA-K2S fusion protein
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; OTHER INFORMATION: sequence for OmpA-K2S fusion protein US-09-987-455-2
                                                                          Score 18; DB 11;
Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Publication No. US20030099974A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
                                                                                     Query Match
Best Local Similarity 100.0%; P. Matches 18; Conservative 0;
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Matches 18; Conservative
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SEQ ID NO 12748
LENGTH: 1415
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APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Roif-Guenther Werner
TITLE OF INVENTION: DAL-Derived tPA or K2S Molecules
TITLE OF INVENTION: DAL-Derived tPA or K2S Molecules
TITLE OF INVENTION: DAL-Derived tPA or K2S Molecules
TITLE OF INIVENTION: DAL-Derived tPA or K2S Molecules
TITLE OF INIVENTION: DAL-Derived tPA or K2S Molecules
TITLE OF INVENTION: DAL-Derived tPA or K2S Molecules
TITLE OF INVENTION: DALE: 2190001
CURRENT APPLICATION NUMBER: US/09/987,455
PRIOR PLILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SSOFWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: DMA-Derived tPA or K28 Molecules
TITLE OF INVENTION: DMA-Derived tPA or K28 Molecules
TILE REPREBNCE: 0652_2190001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT APPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-02-15
PRIOR PLING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SSOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: coding OTHER INFORMATION: sequence for K2S protein
             0; Indels
        0; Mismatches
                                                                                                                                                                                                                                          Sequence 7, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
APPLICANT: Aranya Manosroi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09987455 Publication No. US20030049729A1 GENERAL INFORMATION: APPLICANT: Aranya Manosroi
                                                                                        1 TCTGAGGGAAACAGTGAC 18
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ORGANISM: Artificial Sequence
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        18; Conservative
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Matches 18; Conservative
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LENGTH: 1128
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US-09-987-455-7
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        Matches
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Sequence 5, Application US/09969271
; Sequence 5, Application US/09969271
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));
; APPLICANT: Pfizer Limited (GB and EP (GB) only)
; TITLE OF INVENTION: Pharmaceutical Combinations
; FILE REPRENCE: PCS10951APWE
; CURRENT APPLICATION NUMBER: US/09/969,271
; PRIOR APPLICATION NUMBER: GB 0025473.0
; PRIOR APPLICATION NUMBER: GB 0025473.0
; RIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                          Score 18; DB 14; Length 2509;
Pred. No. 7.7;
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100.0%; Score 18; DB 9; Length 2519;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0: Indela r
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OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CB1
                                                                                                                            Indels
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Patent No. US2002015663A1
GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-004
                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 2635
; OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-144
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                                                                                                                                                                                                                           678 TCTGAGGGAAACAGTGAC 695
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                                                                             100.0%;
; RELEVANT RESIDUES: (1)..(2509)
US-10-193-656-7
                                                                   Query Match
Best Local Similarity 100.
Matches 18; Conservative
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SOFTWARE: PERL Program
SEQ ID NO 144
LENGTH: 2641
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-974-298-144
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APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));
APPLICANT: Pfizer Limited (GB and EP (GB) only)
TITLE OF INVENTION: Pharmaceutical Combinations
FILE REFERENCE: PCS10951APME
CURRENT APPLICATION NUMBER: US/09/969,271
CURRENT FILING DATE: 2001-10-01
PRIOR PILING DATE: 2000-10-17
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                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NY, Tor
TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
FILE REFERENCE: 3810/1J577-US3
CURRENT APPLICATION NUMBER: US/10/193,656
CURRENT FILING DATE: 2002-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/304,461
PRIOR APPLICATION NUMBER: US 60/304,461
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 7

LENGTH. 2509
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DATABASE ENTRY DATE: 1995-03-27
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 1689
                           | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: 1, 2, 3, 1414, 1415
| OTHER INFORMATION: n = A,T,C or G
| US-10-198-846-12748
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09969271
Patent No. US20020098179A1
                                                                                                                                                                                                                                                                                                    625 TCTGAGGGAAACAGTGAC 642
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    ORGANISM: Homo sapiens
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US-09-969-271-6
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nes 18; Conserv
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US-09-969-271-6
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Best Local S:
Matches 18
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HER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 20
HER INFORMATION: EXPRESSED IN HELA,0 SIGNAL = 16+02
HER INFORMATION: EXPRESSED IN HELA,0 SIGNAL = 6.5
HER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 6.5
HER INFORMATION: EXPRESSED IN HONE MARROW, SIGNAL = 25
HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
HER INFORMATION: EXPRESSED IN PT474, SIGNAL = 6.3
HER INFORMATION: EXPRESSED IN PT474, SIGNAL = 5.0
HER INFORMATION: EXPRESSED IN BT471, SIGNAL = 5.0
HER INFORMATION: EXPRESSED IN BT471, SIGNAL = 5.0
HER INFORMATION: EXPRESSED IN BT411, EVALUE 6.00e-82
HER INFORMATION: WISSERROT HIT: PROJSS51.1, EVALUE 6.00e-81
HER INFORMATION: WISSERROT HIT: PROSS52, EVALUE 6.00e-81
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                                   PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 18405
INNORTH: 202
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Job time : 6.07937 secs
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OTHER INFORMATION: MAP TO APO00459.2

OTHER INFORMATION: EXPRESSED IN FETAL I.

OTHER INFORMATION: EXPRESSED IN HELLO,

OTHER INFORMATION: EXPRESSED IN HELLO,

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US-09-864-761-18405
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                 FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
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Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nacleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/109/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 237
LENGTH: 139
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85.6%; Score 15.4; DB 10; Length
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Glycine max
. OTHER INFORMATION: Clone ID: LIB3028-053-Q1-B1-E8
US-09-878-574-237
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CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT PEDLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELING DATE: 2000-02-04

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-06-26

PRIOR PLING DATE: 2000-06-03

PRIOR PLING DATE: 2000-06-03

PRIOR PLING DATE: 2000-06-03

PRIOR PLING DATE: 2000-09-03

PRIOR PLING DATE: 2000-09-03

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-09

PRIOR PLING DATE: 2001-09-03

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                        Sequence 237, Application US/09878574 Patent No. US20020110548A1 GENERAL INFORMATION:
1 TCTGAGGGAAACAGTGA 17
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US-09-878-574-237
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Gaps

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BU156867 BG281371 BU157242 AU135634

BQ877849 BG743550 BG281843

BQ878473

BU157686 AU133204

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BQ676711 AGENCOURT BQ879010 AGENCOURT AU131845 AU131845 BQ682391 AGENCOURT BUS57319 AGENCOURT

BF026008 601670321 BI757143 603028814 BE277041 601178928

ALIGNMENTS

BU179560 AGENCOURT BU160825 AGENCOURT BU145169 AGENCOURT

BU557319 BU179560 BU160825 BU145169

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BQ681189 AGENCOURT BG762691 602734592 BE730286 601563427

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AA376531
LOCUS
DEFINITION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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AA376531 EST88963
BE158218 MR2-HT038
BE173847 CM0-HT056
BE173842 CM0-HT056
                                                           August 18, 2003, 22:44:33 ; Search time 52.6587 Seconds (without alignments) 8307.845 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                 22781392 segs, 12152238056 residues
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Listing first 45 summaries
                                           - nucleic search, using sw model
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BE158218
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Maximum DB seq length: 200000000
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AA376531 21-APR-1997 EST88963 HSC172 cells II Homo sapiens CDNA 5' end similar to plasminogen activator, tissue type (GB:M15518), mRNA sequence. AA376531.1 GI:2028850 Homo sapiens (human) Homo sapiens AA376531 VERSION KEYWORDS SOURCE ORGANISM

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Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=WR2-HT0380-310 100-102-g08&t3=2000-01-31&t4=1) Seq primer: puc 18 forward High quality sequence stop: 335.
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Site_2: Smal; head_neck; Vector: puc18; Site_1: Smal;
No. 196,716 - Individ Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

a 102 c 89 g 31 t
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Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
This sequence was derived from the Fallowing URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-HT0567-010
300-256-g02&t3=2000-03-01&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 374.
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CMO-HT0567-010300-256-g02 HT0567 Homo sapiens cDNA, mRNA sequence.
BEI73847
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1 (bases 1 to 374)

1 (bases 1 to 374)

1 (bases 1 to 374)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matentuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelar, P. S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 18; DB 10;
ilarity 100.0%; Pred. No. 3.9e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                       sapiens"
                                                                                                                                                                                                                      1. .335
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
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PUBMED
COMMENT
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BE173847
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                    FEATURES
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/mol_type="mRNA"
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mRNA sequence.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Gardin, S., Costa, P.F.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                         Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                            For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., F., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
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                                                                                                                                                                                                                                                                      The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                      Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse.
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                                                                                                                                                                                                  Other ESTs: THC167250
Contact: Kerlavage, AR
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100.0%;
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/tissue_type="neuroblastoma"
/lab_host="hH10B (phage-resistant)"
/lab_host="hH10B (phage-resistant)"
/clone_lib="NHH MGC_19"
/note=Torgan: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made_by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE259860 476 bp mRNA linear BST 26-OCT-2000 001154266F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3510113 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 476)
          tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM194 row: d column: 18
High quality sequence stop: 475.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Concact: Robert Strausberg, Ph.D.
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                                                                                                                                                                             Length 378;
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/clone="IMAGE:3510113"
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/dev stref="caon:9606"
/dev stref="caon:9606"
/dov stref="caon:9606"
/dov stref="organ:percentage of the caon of street of
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Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
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CMO-HT0567-010300-256-e04 HT0567 Homo sapiens CDNA, mRNA sequence.
BE173842
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1 (bases 1 to 378)
10 blas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matenkuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-HT0567-010 Seq primer: puc 18 forward High quality sequence stop: 378.
High quality sequence stop: 378.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 10; Length 374; Pred. No. 4e+02;
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Best Local Similarity
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BE173842
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Gaps

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCACAGG(G). Size-selected >500bp for average
insert size 1.8kb. Libzary constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies)."
12 a 165 c 182 g 103 t
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601277221F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618149 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM277 row: m column: 23
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Email: Ggapba-remail.nih.gov

Tissue Procurement: ATC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incytte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM28 row: j column: 06

High quality sequence stop: 612.
                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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100.0%; Score 18; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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//eall line="CK-KI"
//lab_bose="ToploF""
//clone_lib="LiscKKI"
//clone_lib="LiscKKI"
//clone_lib="LiscKKI"
//note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nc. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by GXsyama—Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 519)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE3345/16 ST 21-JUL-2000 601273495F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614782 5', mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Vuseong-gu, Daejeon 305-333, South Korea
Tal: +82-42-860-4410
Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: yongsungemail.kribb.re.kr
Plate: 35 row: D column: 03
High quality sequence stop: 519.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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                                      CB149125
CB149125.1 GI:28131896
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BE386276.1 GI:9331641
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mRNA sequence.
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim, Y.S.
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BASE COUNT ORIGIN

Matches

DEFINITION

BE386276

RESULT 7

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Gaps

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Length 582; Indels

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/lab_host="DH10B (phage-resistant)"
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sl a 183 c 196 g 112 t 2 others
                                                                                                                              BG477932 644 bp mRNA linear EST 21-MAR-2001 602522911F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4641386 5',
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 682)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbe.remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling H.A.G. E. Consortum (LLNL)
CDNA Library Arrayed by: The I.M.A.G. E. Consortum (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G. E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1408 row: e column: 03
High quality sequence stop: 639.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone="IMAGE:4641386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
Contact: Robert Strausberg, Ph.D.
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            439 TCTGAGGGAAACAGTGAC 456
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Best Local Similarity 100.0
Matches 18; Conservative
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47 a 165 c 190 g 103 t 7 others
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Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J.; Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Hesearch Institute, cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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100.0%; Score 18; DB 10; Length 612;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Score 18; DB 9; Length 63
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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/note="Vector: pME18SF13"
/note="Vector: pME18SF13"
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
17El: 81-438-52-3975
Fax: 81-438-52-3986
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Unpublished
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Genomics Laboratory
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AU117078
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KEYWORDS
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/clone="IMAGE:3923602"
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Best Local Similarity
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BG476511
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ORIGIN
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                                                                                                                                                                                                          L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbsr@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM95 row: b column: 04
High quality sequence stop: 614.

High quality sequence stop: 614.
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NIH-MGC http://mgc.nci.nih.gov/.
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Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9760 row: a column: 11
High quality sequence stop: 582.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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Homo sapiens
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Best Local Similarity
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BE895982
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AUTHORS
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                                COMMENT
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/tissue_type="melanotic melanoma"
/lab host="DHLOB (phage_resistant)"
/clone_lib="NIH MGC_20"
/note="Organ: Sitin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/KhoI sites using the following 5'
adaptor: GGCACGG(3). Size-selected >500pp for average
insert size_1:8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
// Sa 189 c 225 g 123 t 1 others
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602522049F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4640172 5',
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 711)
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Tissue Procurement: ATC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1405 row: b column: 13
High quality sequence stop: 711.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Score 18; DB 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:4640172"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TCTGAGGGAACAGTGAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCTGAGGGAAACAGTGAC 18
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                                                                                                                                                                                             Technologies.
225 c
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/done liber Will MGC 122"
//clone liber Will MGC 122"
//clone liber Will MGC 122"
//note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: EccNV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (EccNV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH MGC Library."
                                                                          Email: cgapD8-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G. B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G. E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIS22 row: b column: 22
High quality sequence stop: 738.
Location/Qualifiers
     National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:5208117"
/lab_host="DH108"
                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 19, 2003, 08:29:02 Job time : 59.6587 secs
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Matches 18; Conservative
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lone_line="NIH MGC_112"
/note="Organ: Skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoR1; cDNA made by oligo-dT priming. Directionally. cloned into EcoR1/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and superscript II RT (Life Technologies). Note: this is a
                                                                                                                                  EST 07-NOV-2001
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603058991F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5208117 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: DCTD/DTP,
Tisaue Procurement: DCTD/DTP,
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1875 row: e column: 23
High quality sequence stop: 725.
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11 H-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 711)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                               BM042154 112 bp mRNA linear EST 07-NOV-20 c03615791F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420542 5',
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/mol_type="mRNA"
/db_xref="taxon:9606"
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  573 TCTGAGGGAAACAGTGAC 590
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Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model	nn: August 18, 2003, 19:53:48 ; Search time 277.124 Seconds (without alignments) 9743.047 Million cell updates/sec	:: US-09-987-455-6 ict score: 66 ince: 1 atgaaaagacagctatcgcctaccgtggcccaggcggcc 66	ng table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	hed: 2888711 seqs, 20454813386 residues	Total number of hits satisfying chosen parameters: 5777422
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GenEmbl:\* Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	0829 Sequenc	Sequence	Synthetic	X95747 Synthetic c	ynthetic	Synthetic	AX431271 Sequence	AF268280 Phagemid	AR241678 Sequence	Sequence	AX600065 Sequence	AX554424 Sequence	AX554422 Sequence	AX642149 Sequence	L42764 Staphylococ	AX742885 Sequence	E02814 DNA sequence	ا بد	AX236/21 Sequence IO8200 Sequence 1	152035 Sequence 1	M62710 Synthetic g	AR282580 Sequence	AX022441 Sequence	AXO30798 Sequence AXO34619 Sequence	E01685 hybrid DNA	AF234271 Shigella	lmone]]a		AX191724 Sequence	A08458 pinf 4-49 m	ifici	AJ223122 Artificia	005286 E		;	linear PAT 28-JUN-2002			ıcteria; Enterobacteriales;	Manosroi, A. and Manosroi, J.
CALAMANOS	DB ID	6 AX430829		12 HSIGKLC28	HSIGKLCS	HSIGKLC1	12 HSIGKLG31	6 AX431271	N	6 AR241678	v		6 AX554424 6 AX554413	6 AX554422		1 STAFRA		E02814		6 AX236/21 6 I08200		12 SYNOMPARNA		6 AX022441		6 E01685		STOMPA	AF23426	6 AX191724	1 ECOMPA 6 A08458	2 2	2 ASAK312	1 AE005286	ALIGNMENTS		66 bp DNA Patent WO0240696.	55908		cteria; Gammaproteobacteria;	00
de	Query • Match Length	100.0	100.0	100.0	100.0 705	100.0 711	100.0 711	100.0	100.0	100.0	100.0	100.0	100.0		100.0	97.6	92.7	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	21.6	91.2	91.2	91.2	91.2	91.2	.2 91.2 11641		,	1 from	AX430829 AX430829.1 GI:21655908	<b>≈</b>	Escherichia coli Bacteria; Proteobacteria; Enterobacteriaceae: Esche	Goetz, F., Werner, R.G., Methods for large scal
	Result No. Score															64	21 61.	09	09	909	9	909	9	90	9 6	9	9	9 6	9	96	9	9	43 60	9		T 1 829	z	Z.	SOURCE		REFERENCE 1 AUTHORS G

Patent: WO 0240696-A 1 23-MAY-2002; JOURNAL

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HSIGKLC28 705 bp mRNA linear SYN 29-MAR-2001 Synthetic construct including Homo sapiens immunoglobulin kappa chain (clone: 28).
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Valenta, R.L.S.
Valenta, R.L.S.

Direct Submission

Direct Submission

Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General & Experimental Pathology, General Hospital, Waehringer Guertel 18-20, 1090 Vienna, AUSTRIA

10.705

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 Methods for large scale production of recombinant dna-derived tpa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steinberger, P., Kraft, D. and Valenta, R.
Construction of a combinatorial IgE library from an allergic
patient. Isolation and characterization of human IgE Fabs with
specificity for the major timothy grass pollen allergen, Phl p 5
J. Biol. Chem. 271 (18), 10967-10972 (1996)
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                   or k2s molecules
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llarity 100.0%; Pred. No. 1.4e-11;
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Sequence 6 from Patent W00240650.
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AX431272.1 GI:21656154
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18-20,
Steinberger, P., Kraft, D. and Valenta, R.

Construction of a combinatorial IgE library from an allergic
patient. Isolation and characterization of human IgE Fabs with
specificity for the major timothy grass pollen allergen, Phl p
J. Biol. Chem. 271 (18), 10967-10972 (1996)
8631916
                                                                                                                2 (bases 1 to 705)
Valenta,R.L.S.
Direct Submission
Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General
Experimental Pathology, General Hospital, Waehringer Guertel
1090 Vienna, AUSTRIA
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note="SAC 1 restriction site"

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352. .384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="OMP-A"
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/note="CDR1"
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208. .228
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X9574,
X9574,
X9574,
I GI:1514580
constant region; immunoglobulin; kappa light chain.
synthetic construct
synthetic construct
artificial sequences.
                                                               /trānslation="MKKTAlAlaValAGFATVAQAAELTQSPSSLSASVGDRVTITCR
ASQSILGYLMWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSSGTDFTLTITSLQPDD
FATYYCQQSYJITPRIFGQGTKVEVKRTVAAPEVFIFPPSDEQLKSGTASVCLLNNFY
PREAKVQMKVDNALQSGWSGESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH
QGLSSPVTKIFNRGEC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 705;
 /product="immunoglobulin kappa light chain"
/protein id="QAA65059.1"
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db_xref="REMTREMBL:CAA65059"
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100.0%; Pred. No. 1.6e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         7. 72
gene="OMP-A"
note="SAC 1 restriction site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="OMP-A"
/note="PCR-primer sequence"
201 c 172 g 148 t
                                                                                                                                                                                                                                                                           note="PCR-primer sequence"
                                                                                                                                                                                note="leaderpeptide gene"
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/gene="OMP-A"
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'gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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                                                                                                                                                                                                                                                                                                                                                                                                                            note="FR2"
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66; Conservative
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HSIGKLC5
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CRASHSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTLSSLQP
BDFANYYQQESFSPSGTFGQTKVEIKRTVAASSLQSGVPSRFSGSGSGTDFTLTLSSLQP
FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKLYACEV
THQGLSSPVTKSFNRGEC"
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Synthetic construct including Homo sapiens immunoglobulin kappa
chain (clone: 31).
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constant region; immunoglobulin; kappa light chain.
synthetic construct
synthetic construct
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Steinberger, P., Kraft, D. and Valenta, R.
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/gene="OMP-A"
/note="CDR1"
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/gene="OMP-A"
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|qene="OMP-A"
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/gene="OMP-A"
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/gene="OMP-A"
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note="FR2"
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/gene="OMP-A"
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Sheet Good 66; Conservative
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Synthetic construct including Homo sapiens immunoglobulin kappa
chain (clone: 14).
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Submitted (19-FBB-1996) R.L.S. Valenta, Institute of General &
Experimental Pathology, General Hospital, Waehringer Guertel 18-20,
1090 Vienna, AUSTRIA
                                                                                                                                                                                                                                             1 ATGAAAAAGACAGCIATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTGGCCCAG 60
                                                                                                                                                                                                                                                                Steinberger, P., Kraft, D. and Valenta, R.
Construction of a combinatorial IgE library from an allergic
patient. Isolation and characterization of human IgE Fabs with
specificity for the major timothy grass pollen allergen, Phl p 5
J. Biol. Chem. 271 (18), 10967-10972 (1996)
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constant region; immunoglobulin; kappa light chain.
synthetic construct
synthetic construct
artificial sequences.
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                         385. .702
/gene="OMP-A"
/note="kappa constant region"
661. .705

    .66
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    /db_xref="taxon:562"

                                                                                j61. ./vo
/gene="OMP-A"
/note="PCR-primer sequence"
'n1 c 181 g 150 t
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/db_xref="taxon:32630"
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clone_lib="pcomb3H"
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 'gene="OMP-A"
                'note="FR4"
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Valenta, R.L.S.
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66; Conservative
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HSIGKLC14
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Goetz,F., Werner,R.G., Tayapiwatana,C., Manosroi,A. and Manosroi,J. Methods for large scale production of recombinant dna-derived tpa or k2s molecules
Patent: WO 0240650-A 2 23-MAY-2002;
BOEHRINGER INGELHEIM INT (DE)
                                                                                                                                                                                                                                                                                                                                                                                PAT 28-JUN-2002
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                                                                                                                                                                                     Gaps
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Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                     ch 100.0%; Score 66; DB 12; Similarity 100.0%; Pred. No. 1.6e-11; 66; Conservative 0; Mismatches 0;
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                     391. .708
//gene="OMP-A"
/note="kappa constant region"
667. .708
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                                                                                                                                                                                                                                                                                                                                                                              AX431268 1128 bp
Sequence 2 from Patent WO0240650.
AX431268
                                                                                                           179 g
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                                                                                            /note="PCR-primer
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/gene="OMP-A"
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KRAQSISSYLNMYQQKPRARKLITAASSLGSGVBRRFSGSGSGGTPTLTISSLQP
EDRATYCQQSHSFPTFGGGTNLETKRTVAAPSVPTPPPSDBQLKGSGTASVVCLLNN
FYPREAKVQMKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEN
                                                                                          2 (bases 1 to 711)
Valenta, K.L.S.
Direct Submission
Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General &
Experimental Pathology, General Hospital, Waehringer Guertel 18-20,
1090 Vienna, AUSTRIA
Location/Qualifiers
Construction of a combinatorial IgE library from an allergic patient. Isolation and characterization of human IgE Fabs with specificity for the major timothy grass pollen allergen, Phl p 96210038 [18], 10967-10972 [1996]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/db_xref="REMTREMBLE.CAA65061"

    711 /organism="synthetic construct"
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gene="OMP-A"
note="SAC 1 restriction site"

    .66
    /organism="Escherichia coli"
/mol_type="mRNA"
    /db_xref="taxon:562"

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note="PCR-primer sequence"
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1. .711
/gene="OMP-A"
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clone="31"
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/gene="OMP-A"
/note="FR1"
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|gene="OMP-A"
|note="CDR1"
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gene="OMP-A"
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/gene="OMP-A"
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andak, LD. Wirsching, P., Lerner, R.A. and Gao, C.
Methods for display of heterodimeric proteins on filamentous phage using PVII and plx, compositions, vectors and combinatorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-MAY-2000) Department of Molecular Biology, BCC-526, Scripps Research Institute, 10550 N. Torrey Pines Rd., La Jolla, 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            artificial sequences, vectors.

1 (bases 1 to 3758)

Rader, C. and Barbas, C.P. III.

(in) PHAGE DISPLAY, A LABORATORY MANUAL. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, USA (2000), In press 2 (bases 1 to 3758)

Rader, C. and Barbas, C.F. III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGABABAGACAGCTATCGCGATTGCAGTGGCACTGGCTTTCGCTACCGTGGCCCAG
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Phagemid cloning vector pComb3X, complete sequence.
AF268281
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Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 66; Conservative 0; Mismatches 0;
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/db_xref="taxon:137786"
_896 c 959 g 96
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799 c 891 g
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 Methods for large scale production of recombinant dna-derived tpa
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artificial cloning vector pComb3H
artificial sequences; vectors.

1 (bases I to 3394)
(in) PHAGE DISPLAY, A LABORATORY MANUAL. Cold Spring Harbor Laboratory Press, C. Cold Spring Harbor.

2 (bases I to 3394)
Barbas, C.F. III.

2 (bases I to 3394)
Brader, C.F. III.
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783 c 876 g 873 t
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ive 0; Mismatches 0; Indels
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             or k2s molecules
Patent: WO 0240650-A 5 23-MAY-2002;
BOEHRINGER INCELHEIM INT (DE)
Location/Qualifiers
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Patent: WO 02462394 A 60 13-UN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
Location/Qualifiers
1. :5149
/ organism="synthetic construct"
/ mol_type="genomic DNA"
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100.0%; Pred. No. 1.8e-11;
tive 0; Mismatches 0;
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Matches 66; Conservative 0; Mismatches 0;
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                                                                                                                    Bowdish, K.S. and Barbas-Frederickson, S.
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Patent: WO 0246434-A 8 13-JUN-2002,
ALEXION PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 60 from Patent WO0246238.
AX600065
Sequence 8 from Patent W00246434.
AX591634
AX591634.1 GI:27950030
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RESULT 15 AX554424

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Patent: WO 024436-A 12 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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100.0%; Score 66; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 66; Conservative 0; Mismatches 0;
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/noTe="plasmid"
Sequence 12 from Patent W00246436.
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Copyright (c) 1993 - 2003
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Listing first 45 summaries
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## ALIGNMENTS

Tissue plasminogen activator; tPA; kringle 2 serine protease; stroke; KSS; cardiaci infarction; acute myocardial infarction; pulmonary embolism; artery occlusion; deep vein thrombosis; blood clotting; thrombolytic; cerebroprotective; cardiant; ompA; gene; ds. Escherichia coli ompA peptide encoding DNA. Location/Qualifiers
1..66
/\*tag= a
/product= "OmpA peptide"
/note= "No stop codon"
/partial AAD40615 standard; DNA; 66 BP (first entry) Escherichia coli. 30-0CT-2002 AAD40615; Key RESULT 1 AAD40615 

07-NOV-2001; 2001WO-EP12857. 14-NOV-2000; 2000GB-0027779.

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23-MAY-2002

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                                                                                                                                                                   secreted, active, correctly folded, recombinant tissue plasminogen activator (LPA), Kringle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants. Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary-embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain, peripherally occluded arteries. coronary artery occlusion, deep vein thrombosis or related diseases associated with unwanted blood clotting. The present sequence is a DNA fragment encoding Escherichia coli OmpA peptide.
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                                                                                  Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
                                                                                                                                                           present invention relates to a method of producing extracellularly
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                Tayapiwatana C, Manosroi J, Manosroi A;
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100.0%; Pred. No. 2.1e-14;
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           (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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                                                                                                                                       Claim 8; Page 30; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD38987 standard; DNA; 66 BP.
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                                Goetz F,
                                                    WPI; 2002-519376/55
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                                                               P-PSDB; AAE25035
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                                                                                                                   peptide OmpA
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The invention relates to a method for producing recombinant DNA-derived heterologous protein in prokaryotic cells, where the heterologous protein is secreted extracellularly as an active and correctly folded protein and the prokaryotic cell contains and expresses a vector comprising the DNA coding for the heterologous protein operably linked to the DNA coding for the signal peptide OmpA or its functional derivative. The method is useful for commercial large-scale production of heterologous proteins, e.g. KZS (Kringle 2 plus serine protease), in prokaryotic cells, and is generally applicable in the expression of several different proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue plasminogen activator; tPA; kringle 2 serine protease; stroke; K2S; cardiac infarction; acute myocardial infarction; pulmonary embolism; artery occlusion; deep vein thrombosis; blood clotting; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides which do not require mammalian glycosylation in prokaryotic host cells. The method may also be used to obtain DNA sequences of a protein of interest to be expressed from databases and cloned for use. The present sequence is Escherichia coli OmpA DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTTCGCTACCGTGGCCCAG
Producing recombinant DNA-derived kringle 2 plus serine protease, comprises using a prokaryotic cell expressing a vector having a DNA coding for a heterologous protein operably linked to a DNA coding for the signal peptide OmpA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OmpA-K2S fusion protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tayapiwatana C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..1128
                                                                                                                                                                          Claim 9; Page 23; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD40614 Standard; DNA; 1128
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1es 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD40614;
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                                                                                                             The present invention relates to a method of producing extracellularly secreted, active, correctly folded, recombinant tissue plasminogen activator (tPA), rkingle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants. Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vein thrombosis or related diseases associated with unwanted blood clotting. The present sequence is a DNA encoding a fusion protein comprising OmpA and K2S protein.
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                                                                                                                                                                                                                                                                                                                                                                 AIGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTGGCCCAG 60
                        rroducing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA
                                                                                                                                                                                                                                                                                                                                         Erythrocyte; Hepatitis B; dual-specific antibody; surface antigen; ds
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                      100.0%; Score 66; DB 24; Length 1128; 100.0%; Pred. No. 4.3e-14;
                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic engineering double specific antibody and its use
                                                                                                                                                                                                                                                                               Sequence 1128 BP; 238 A; 332 C; 332 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                         Claim 7; Page 30; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ57599 standard; DNA; 1574 BP.
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                                                                                                                                                                                                                                                                                                                             66; Conservative
WPI; 2002-519376/55.
P-PSDB; AAE25034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   851
which can be used as the test reagent to detect the surface antigen of hepatitis B in blood. The dual-specific antibody is prepared by recombination technique in gene engineering. The recombination technique includes reforming the surface antigen to resist against erythrocyte and hepatitis B to become hybrid antibody genes by shortening the same expression vector. The gene product can be directly extracted from the superinatant of bacterial culture liquid. Its advantages are low
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAAAAAGCTATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTGGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 66; DB 21; Length 1574; 100.0%; Pred. No. 4.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                             Sequence 1574 BP; 395 A; 390 C; 419 G; 370 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3450 BP; 873 A; 799 C; 891 G; 887 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Filamentous phage; protein display; pVII; pIX; combinatorial antibody library; ds.
                                                                                                                                                                                                                                                     cost, quick detection and simple operation.
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC66993 Btandard; DNA; 3450 BP.
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0%;
Matches 66; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
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construct of the MT4 Fab display phagemid expression vector, pMT4-3 (see also AAQ92540), used in the invention for the production of synthetic human Fab antibodies against gpl20 of HIV.

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Sequence 4691 BP; 1170 A; 1171 C; 1232 G; 1118 T; 0 other;

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Gaps

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0; Indels

; Pred. No. 6.1e-14; 0; Mismatches 0;

Score 66; Pred. No. 6

100.0%;

Query Match
Best Local Similarity
Local 66; Conservative

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Length 4691;

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This sequence represents the pComb3 phagemid expression vector. This vector has been designed to allow for anchoring of expressed proteins on the bacteriophage coat protein 3. Gene III of filamentous phage encodes the bacteriophage coat protein, cplII (cp3), which is expressed prior to extrusion in the phage assembly process on a bacterial comparison and accumulates on the inner membrane facing into the periplasm of express various mutagenised human Fab's which comprise heavy and light convariable regions which bind to HIV gp120. pComb3 allows for both surface display and soluble forms of the Fabb. The vector was designed for the cloning of combinatorial Fab libraries. pComb consists of a DNA molecule cloning of combinatorial Fab libraries. pComb consists of a DNA molecule coloning vocassettes to express one fusion protein, Fd/cp3, and one soluble protein, the light chain. The finished vector comprises, prometer/operator sequences, a NoII restriction site, a ribosome binding site (RBS), a PelB leader, a spacer region, a cloning region bordered by 5' XhoI and 3' SpeI restriction sites, the tether sequence, the sequences encoding bacteriophage cp3 followed by a stop codon, a NeII restriction site between the two cassettes, and a second lac2 promoter/operator cegenon, a cloning region bordered by 5' SacI and 3' SpeI restriction control RBS, a PelB leader, a spacer region, a cloning region bordered by 5' SacI and 3' SpeI restriction control RBS, a PelB leader, a spacer cegion, a cloning region bordered by 5' SacI and 3' SpeI restriction control RBS, a PelB leader, a spacer region, a cloning region bordered by 5' SacI and 3' SpeI restriction control stop sequences and a second NotI restriction site. The pComb3 expression control stop sequences and a second NotI restriction site. The pComb3 expression vector forms the basic
                           2667 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGTTTCGCTACCGTGGCCCAG 2726
1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTTCGCTACCGTGGCCCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pComb3; phagemid expression vector; bacteriophage; coat protein 3; Gene III; filamentous phage; minor phage coat protein; cpIII; cp3; bacterial membrane; periplasm; E. coli; human; Fab; HIV; gpl20; combinatorial Fab library; cassette; Fd/cp3; lacZ promoter/operator; ribosome binding site; RBS; PelB leader; spacer; tether sequence; MT4; pMT4-3; antibody; ss; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic human neutralising monoclonal antibodies to human
immunodeficiency virus - used for diagnosis and immuno:therapy of
HIV-induced disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 185-188; 249pp; English.
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                                                                                                                                                                                                                                                                 AAQ92546 standard; DNA; 4691 BP.
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93US-0139409.
94US-0233619.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               pComb3 expression vector.
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19-OCT-1993;
26-APR-1994;
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The present invention describes an immunoglobin molecule or its fragment (1) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoletin (BPO) or thrombopoletin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (1) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoletic cells, and a stimulator of haematopolesis. (1) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (1) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet production. (1) with a region where amino acid residues corresponding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or
                                                                                                                                                                                                                                                                             TPO; BPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renshaw M;
                                                                                                                                                                                                                                         Plasmid pRLB nucleotide sequence SEQ ID NO:60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 6A-C; 113pp; English.
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                                                                                                                               BP.
                                                                                                                              ABQ73372 standard; DNA; 5149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-2001; 2001WO-US47656.
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29-MAY-2001; 2001US-294068P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-2000; 2000US-251448P.
                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALEX-) ALEXION PHARM INC.
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                                    2671 GCGGCC 2676
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99 ວ່ວອີວ່ວອີ 19
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200246238-A2.
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                      01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                    ABQ73372;
                                                                                                                                                                                                                                                                                                                                      gene; ds.
                                                                                             RESULT 7
                                                                                                                ABQ73372
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a portion of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with hammatopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, disorders or treatments related to the suppression of hammatopoiesis. ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used
                                                                                                                                                                                                                   1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTGGTTTCGCTACCGTGGCCCAG
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel pComb family phagemid comprising a nucleic acid encoding a dimerization domain, useful for producing antibody fragments which require dimerization in order to crosslink for activation of target
                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "the CDS does not include a start codon"
                                                                                                                                                                    DB 24; Length 5149;
                                                                                                                                        Sequence 5149 BP; 1279 A; 1244 C; 1372 G; 1254 T; 0 other;
                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vector; phagemid; pRL8; pComb; dimerisation domain; Jun;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
note= "light chain stuffer region"
1968..4337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "heavy chain stuffer region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Jun dimerisation domain"
                                                                                                              in the exemplification of the present invention.
                                                                                                                                                                                 6.2e-14;
                                                                                                                                                                          100.0%; Pred. nc.
                                                                                                                                                                 100.0%; Score 66; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leucine zipper; antibody; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barbas-Frederickson S;
                                                                                                                                                                                                                                                                                                                                                                        ABN84077 standard; DNA; 5149 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2001; 2001WO-US46514.
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                                                                                                                                                                               Best Local Similarity 100.
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phagemid vector pRL8.
                                                                                                                                                                                                                                                                                                   2671 GCGGCC 2676
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P-PSDB; ABB79463.
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misc_feature
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"CH1, His6 tag, HA tag, and gene III amino acid
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                     The present sequence is of plasmid pLR8, a pComb vector family member. pLR8 was constructed by insertion of a PCR fragment containing a flexible linker (murine kappa hinge region) followed by a Jun leucine zipper dimerisation domain into a pRL4 backbone that had been treated to remove the stuffer region. The resulting construct was then cut with restriction endonucleases to replace serv with a pRL4 stuffer region for the light and heavy chain. The vector is useful in the production of biologically active proteins biological activity. It can also be used in the production and screening of librarismation of single chain antibodies is accomplished by the presence of the Jun leucine zipper domain, which is responsible for protein-protein interactions. Subcloning to pRL8 individually or en masse following FACS sorting or panning allows expression, e.g., of dimeric soluble Fabs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid, vector; replication, expression, foreign genetic, bacteria; cyanobacterium; Bscherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT; pRL5-CAT; pRL5 bsi-CAT; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                  "Kappa constant region amino acid sequence"
                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                     100.0%; Score 66; DB 24; Length 5149; 100.0%; Pred. No. 6.2e-14; tive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                             Sequence 5149 BP; 1279 A; 1244 C; 1372 G; 1254 T; 0 other;
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Disclosure; Fig 8A-C; 17pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pRL5 nucleic acid sequence.
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Matches 66; Conservative (
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4740..5651
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                                                                                   (ALEX-) ALEXION PHARM INC
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Matches 66; Conservative
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                                                                                                                                                               information
                           13-JUN-2002
                                                                                                     Bowdish KS,
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product= "CH1, His6 tag, HA tag, and gene III amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid; vector; replication; expression; foreign genetic; bacteria; cyanobacterium; Escherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT; pRL5-CAT; pRL5 bsi-CAT; gene; ds.
                                                                                                                                                                                                                                                                                              "Kappa constant region amino acid sequence"
                                                                                                                                                                                                                                                                           Gaps
                                                                                            plasmid useful in cloning and expression of foreign genetic
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                                                                                                                                                                                                                                                        Length 5683;
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                                              Mcwhirter J;
                                                                                                                                                                                                                                      Sequence 5683 BP; 1337 A; 1495 C; 1540 G; 1311 T; 0 other;
                                                                                                                                                                                                                                                                          0; Indels
                                                                 WPI; 2002-537570/57.
P-PSDB; AAO22536, AAO22537, AAO22538, AAO22539, AAO22542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "CAT amino acid sequence"
                                                                                                                                                                                                                                                                 6.4e-14;
                                                                                                                                                                                                                                                         DB 24;
                                             Barbas-frederickson S, Wild M,
                                                                                                                                                                                                                                                       100.0%; Score 66; DB
100.0%; Pred. No. 6.4.
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pRL5 CAT nucleic acid sequence.
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1013..1672
                                                                                                                        Claim 1; Fig 4A-E; 39pp; English.
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         08-DEC-2000; 2000US-254411P.
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/*tag= b
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                           (ALEX-) ALEXION PHARM INC.
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Matches 66; Conservative
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                                                                                                       information
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                                              Bowdish
                                                                                            Novel
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/product= "Kappa constant region amino acid sequence"
4298..4363
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                                                                                                                                                           Mcwhirter J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6122 BP; 1449 A; 1571 C; 1639 G; 1463 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                             WPI; 2002-537570/57.
P-PSDB; AAO22535, AAO22536, AAO22537, AAO22539, AAO22539
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                                                                                                                                                         Wild M,
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; Pred. No. 6.5e
0; Mismatches
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                                                                                                                                                           Barbas-frederickson S,
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                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 7A-E; 39pp; English.
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/product= "C
3050..3115
07-DEC-2001; 2001WO-US46516.
                                                      08-DEC-2000; 2000US-254411P.
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                                                                 misc_signal
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                                          promoter
                                                                                          RBS
                                                                                                         CDS
                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                         SDS
  The invention relates to a plasmid with a nucleic acid sequence of 6122, 6125, or 5683 base pairs fully defined in the specification. The invention more specifically relates to novel vectors capable of replication and expression of foreign genetic information in bacteria, such as, for example, cyanobacterium and B. coli. The new vectors have been designed to overcome certain drawbacks of the pCombix plasmid. These new vectors include pRLS, pRLS-CAT, pRLS asc-CAT and pRLS bsi-CAT. This polymucles is accordance of the plasmid pRLS bsi-CAT nucleic acid
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                                  acid
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                                  amino
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                              Novel plasmid useful in cloning and expression of foreign genetic
                               "CH1, His6 tag, HA tag, and gene III
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/note= "the CDS does not include a stop codon"
1013..1672
                                                                                                                                                                                                                                                                                                                       Length 6122;
        "pel B leader amino acid sequence"
                                                                                                                                                                                                                                                                                                      Sequence 6122 BP; 1447 A; 1571 C; 1641 G; 1463 T; 0 other;
                                                                                                                                         Mcwhirter J;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                AA022541
                                                                                                                                                                                                                                                                                                                             6.5e-14;
hes 0;
                                                                                                                                                                                                                                                                                                                        DB 24;
                                                                                                                                                              P-PSDB; AA022535, AA022536, AA022538, AA022539,
                                                                                                                                        Wild M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pTL5-CAT; vector; antibody; gene; ds.
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                       Score 66;
Pred. No.
                                                                                                                                                                                                      Disclosure, Fig 11A-E; 39pp; English.
                                                                                                                                       Barbas-frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN84078 standard; DNA; 6122
               5179..6090
/*tag= e
/product= "C
                                                                                       07-DEC-2001; 2001WO-US46516
                                                                                                      08-DEC-2000; 2000US-254411P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               '*tag= a
'partial
/*tag= d
/product=
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                                                                                                                       (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                       sequence of the invention.
                                       sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 66, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391..800
                                                                                                                                                                                                                                                                                                                                                                                                     3110 GCGGCC 3115
                                                                                                                                                      WPI; 2002-537570/57
                                                                                                                                                                                                                                                                                                                                                                                      61 GCGGCC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pRLS-CAT.
                                                       WO200246436-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                      Bowdish KS,
                                                                       13-JUN-2002
                                                                                                                                                                                        information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN84078;
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOS
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TTTTTTXSXXXXBXTTTTTT
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Plasmid for in situ production of genes, comprises two template annealing sequences, such as downstream primer and upstream collar sequence and a restriction site located between the annealing sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not include a start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "pelB leader"
/note= "the CDS does not include a stop codon"
4365..5147
                                                                                                                                                                                                                                                                                                                                                                                           product= "OmpA leader"
note= "the CDS does not include a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= h
note= "light chain variable region stuffer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= k
'note= "heavy chain variable region stuffer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Linker-His tag-HA tag"
/note= "the CDS does not include a start
5557..6090
/product= "Chloramphenicol transferase"
complement (2052..2651)
                                                                                                                                                   'note= "lac promoter"
3009..3029
                                                                                                                                                                                                                                       site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene= "Gene III"
/note= "the CDS does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4A-T; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= 1
note= "Kappa Cns"
                                                                                                                                                                                                         '*tag= e
'note= "lac rep
                                                   '*tag≈ c
'note= "ori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-2001; 2001WO-US47452.
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                                                                                                                                                                                                                                                                                                                                          partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           951..4269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3485..5556
                                                                                                  831..3046
                                                                                                                                                                                                                                                             036..3039
                                                                                                                                                                                                                                                                                                              3050.33115
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                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid, vector; replication; expression; foreign genetic; bacteria; cyanobacterium; Escherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT; pRL5-CAT; pRL5 bsi-CAT; gene; ds.
                                                                                                                                                                                                                                                                  ведиепсе "
                                                                                                                                                                                                                                          Gaps
           mENA. The plasmids are engineered to contain 2 template annealing sequences (see ABN84079-80 and ABN84082-83), i.e. a downstream primer that anneals to a first portion of a nucleic acid template, e.g. mENA encoding at least a portion of an antibody, an upstream collar sequence that anneals to a second portion of the template, and at least 1 restriction site located between the 2 template annealing sequences. A single-stranded DNA plasmid vector is produced containing a nucleic acid encoding at least a portion of a polypeptide, e.g. a light chain and/or a heavy chain of an antibody. This vector can be transformed into a host cell and
directly incorporated into the plasmid by reverse transcription of mRNA. The plasmids are engineered to contain 2 template annealing
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                             Length 6122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Kappa constant region amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "pel B leader amino acid sequence
                                                                                                                                                                                Sequence 6122 BP; 1449 A; 1571 C; 1639 G; 1463 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barbas-frederickson S, Wild M, Mcwhirter J;
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CAT amino acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Omp A leader amino acid
                                                                                                                                                                                                           Score 66; DB 24;
Pred. No. 6.5e-14;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pRL5 CAT-Asc nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                       ,
                                                                                                                                                                                                                                                                                                                                                                                                                      AAL41114 standard; DNA; 6125 BP.
                                                                                                                                                                                                          100.0%;
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/product=
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/product=
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                                                                                                                                                                                                                                                                                                                                                   3110 GCGGCC 3115
                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                         61 GCGGCC 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2002
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 886666666666666888
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6125, or 5683 base pairs fully defined in the specification. The invention more specifically relates to novel vectors capable of replication and expression of foreign genetic information in bacteria, such as, for example, cyanobacterium and B. coli. The new vectors have been designed to overcome certain drawbacks of the pComb3x plasmid These polynucleotis include pRL5, pRL5-CAT, pRL5 asc-CAT and pRL5 bs1-CAT. This sequence of the invention.
                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                    The invention relates to a plasmid with a nucleic acid sequence of 6122,
                                                                                                                                                                                                                                                                                                                                          Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAb; immunoreaction; neutralisation; passive immunotherapy; tetanus toxin; alkaline phosphatase; phoA; ss; cyclic.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic human neutralising monoclonal antibodies to human immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-induced disease
                                                 Novel plasmid useful in cloning and expression of foreign genetic
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                               ; Score 66; DB 24; Length 6125;
; Pred. No. 6.5e-14;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                          Sequence 6125 BP; 1447 A; 1573 C; 1644 G; 1461 T; 0 other;
                     P-PSDB; AAO22535, AAO22536, AAO22538, AAO22539, AAO22540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lerner RA;
                                                                                           Claim 1; Fig 9A-E; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ92547 standard; DNA; 6166
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94US-0233619.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 66; Conservative
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           2002-537570/57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-1993;
26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1995.
                                                                 information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ92547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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modified version of the pagenid expression vector, prombs given in AAQ92546. pho-TT provides for the expression of soluble Fabs which are secreted into the periplasmic space which is regulated from the alkaline phosphatase (phoA) promoter. This plasmid was used within the scope of the invention to express various mutagenised human Fab's which comprise heavy and light variable regions which bind to HIV 99120. pho-TT consists of a DNA molecule having two cassettes to express two soluble proteins a heavy chain and a light chain. The vector comprises, operatively linked 5' to 3', a first cassette consisting of the phoA promoter/operator sequences, an ECORI restriction site, a ribosome binding site (RBS), an OmpA leader, a Sfil restriction site, a spacer sequences, an moral residual and 3' Spal restriction cassette consisting of an expression control RBS, a PelB leader, a human consensus amno terminus site between the two cassettees, and a second cassette consisting of an expression control RBS, a PelB leader, a human consensus amno terminus site between the two cassettees and a Notle sequence BVOLLE, a cloning region bordered by 5' XNOI and 3' Spal restriction site.

Collowed by a Sfil site, expression control stop sequences and a NoI restriction site. The pbho-TT expression vector contains a light restriction site. The pho-TT expression of the heavy chain stuffer that is 1200 bp in length and a heavy chain stuffer that is 1200 bp in length and a heavy chain stuffer that is 1200 by in length and a heavy chain stuffer that is 1200 by in length and a heavy chain stuffer that is the contains and light chain variable domains of a contains and solutions and a second case and a second case and a substance and a light chain stuffer second case and a light chain variable domains of a
This sequence represents the expression vector, pPho-TT which is a modified version of the phacemid expression vector modified version of the phacemid expression vector.
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Length 6166; Sequence 6166 BP; 1416 A; 1706 C; 1629 G; 1415 T; 0 other; ch 100.0%; Score 66; DB 16; Similarity 100.0%; Pred. No. 6.5e-14; 66; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches

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0; Gaps

0; Indels

4541 ATGAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGCTTTCGCTACCGTGGCCCCAG 4600 셤

4601 GCGGCC 4606 61 GCGGCC 66 ò

AAQ10569

AAQ10569 standard; DNA; 73 BP. AAQ10569; CXSXLLXBXLXBXLXBXBXBXSXXXXXXCCXCX

Omp A signal peptide-encoding sequence

(first entry)

26-APR-1991

Mirabilis antiviral protein; MAP; Omp A signal sequence; ds.

Mirabilis jalapa.

EP414134-A.

27-FEB-1991

90EP-0115718, 16-AUG-1990; 89JP-0210767 17-AUG-1989;

(NISB ) JAPAN TOBACCO INC.

Gene encoding Mirabilis Antiviral Protien and OmpA signal peptide for mass-prodn. of extracellular MAP. WPI; 1991-059386/09.

Noma

Matsumoto T,

Tsuge H,

Habuka N, Akiyama K,

Claim 1; page 8; 15pp; English

This Omp A signal peptide-encoding sequence is contained in a

recombinant plasmid, flanked on its 3' side by a Mirabilis antiviral protein (MAP) gene. The plasmid is used to transform E.coli host cells in the large-scale prodn. of MAP. The 5' end overhangs the 3' end of the complementary strand by TA and the 5' end of the complementary strand overhangs the 3' end of this sense strand by CTAG. See also AAQ10568. 8X88888XX

Sequence 73 BP; 16 A; 20 C; 21 G; 16 T; 0 other;

Gaps . 0 Length 73; Indels DB 12; Score 60.2; DB 12 Pred. No. 2.7e-12; 0; Mismatches 3 Query Match
Best Local Similarity 95.4%;
Matches 62; Conservative

9 2 ATGABABAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCAG 61 셤 ઠ

61 GCGGC 65

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SCCGC

Search completed: August 18, 2003, 23:28:53 Job time : 24.2513 secs

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Sequence 10, Appl
Sequence 1, Appli
Patent No. 5223407
Sequence 1, Appli
Sequence 1, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
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Sequence 2, Appli
Sequence 10, Appl
Sequence 1, Appli
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Sequence 51, Appl
                                                                                                            August 18, 2003, 22:51:23; Search time 5.16534 Seconds (without alignments) 5639.757 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed
and is derived by analysis of the total score distribution.
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Sequence 7
Sequence 7
Sequence 5
Sequence 5
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Sequence 5
Sequence 5
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
// cgn2_6/ptodata/2/ina/5B_COMB.seq:*
// cgn2_6/ptodata/2/ina/6A_COMB.seq:*
// cgn2_6/ptodata/2/ina/6B_COMB.seq:*
// cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
// cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
// cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
// cgn2_6/ptodata/2/ina/pacxfiles1.seq:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-08-828-741B-1.

US-09-160-567-1

US-09-10-299-1

US-08-880-829-21

US-08-880-829-21

US-08-880-81-10

US-09-100-567-7

US-09-110-299-7

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US-08-264-485-23
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                                                                                                                                                                                                                                                                                                                                  569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
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Maximum DB
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APPLICANT: Janda, Kim D
APPLICANT: Janda, Kim D
APPLICANT: Janda, Kin D
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Changahou
TITLE OF INVENTION: WETHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON
TITLE OF INVENTION: FILAMENTOUS PHAGE USING PVII AND PIX, COMPOSITIONS,
TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
FILE REFERENCE: TSR0305S
CURRENT APPLICATION NUMBER: US/09/318,786
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 39
SOFTHARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 3450
Patent No. 5187153
Patent No. 5223482
Sequence 5, Appli
Sequence 5, Appli
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                                                                                               Sequence 1, 1 Sequence 3, 1 Sequence 3, 1 Sequence 3, 2 Sequence 5, 2 Sequence 5, 3 Sequence 7, 4 Sequence 4, 4 Sequence 6, 8 Sequence 6, 8 Sequence 12, 5 S
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US-08-591-632-43
Sequence 43, Application US/08591632
Sequence 43, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
PAPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Righard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: US-09-318-786-20
                       5223482-26
US-09-518-498-5
US-09-518-498-1
US-09-518-498-3
US-09-518-869-1
US-09-618-869-1
US-09-618-869-1
US-09-618-869-1
US-09-618-869-1
US-08-264-485-5
US-08-264-485-5
US-08-264-485-5
US-09-204-1968-4
US-08-648-262-7
US-08-648-262-7
US-08-648-262-7
US-08-648-262-7
US-08-213-138-12
US-08-215-138-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09318786 Patent No. 6472147 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 66, Conservative
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  TYPE: DNA
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APPLICANT: Barbas, Carlos F.
APPLICANT: Barbas, Carlos F.
APPLICANT: Barbas, Carlos F.
APPLICANT: Berner, Mighard A.
TITLE OF INVENTION: STWITHETIC HUMAN NEUTRALIZING MONOCLONAL
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNOBEFICIENCY VIRUS
NUMBER OF SEQUENCES:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 66; DB 4; Length 4691;
100.0%; Pred. No. 1.1e-13;
tive 0; Mismatches 0; Indels (
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APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-U1-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 19-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REGISTRENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (619) 784-2937
                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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Best Local Similarity 100.0%;
                                ZIP: 92037
COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy
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STATE: C/
COUNTRY:
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Burton, Dennis R.
Lerner, Righard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNOBERICIENCY VIRUS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4691;
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                                         STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8 CITY: La Jolla
ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 66; DB 3; I Similarity 100.0%; Pred. No. 1.1e-13; 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       PRELICATION NUMBER: US/08/591,632
PRICA PAPLICATION DATE: 19-0CT-1994
PRICA PAPLICATION DATE: APPLICATION DATE: APPLICATION NUMBER: PCT/US94/11907
PILING DATE: 19-0CT-1994
PRICA APPLICATION DATA: APPLICATION NUMBER: US 08/308,841
PRICA APPLICATION DATA: PRICA APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/233,619
PRICA APPLICATION DATA: APPLICATION NUMBER: US 08/139,409
PRICA APPLICATION DATA: APPLICATION NUMBER: US 08/139,409
PRICA APPLICATION NUMBER: US 08/139,409
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET UNBER: TSI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                Patent Counse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4691 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2671 GCGGCC 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 66; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCGGCC 66
                                                                                                                                                      USA
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US-09-611-451-43
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                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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100.0%; Score 66; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: BIRCH, STEWART, KOLASCH, & BIRCH
8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                             TSRI 332.3
               APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-1992
20-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HABUKA, No. 5340732iyuki APPLICANT: HYANO, Masashi APPLICANT: MATSUMOTO, Takashi APPLICANT: NOMA, Masana TITLE OF INVENTION: ANTIVIRAL PROTEIN NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22042
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pair-
                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07854845B
                                                                                                                                                                                                                                                                    TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE DOCKET NUMBER: 4:
TELECOMMUNICATION INFORMATION
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 8110 Gateho
CITY: Falls Church
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1601 GCGCCC 4606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GCGGCC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5340732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-611-451-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-07-854-845B-2
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Burton, Dennis R.
Lerner, Righard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: The Scripps Research Institute, Office of Patent Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 66; DB 3; Length 6166; 100.0%; Pred. No. 1.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-011-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
                                 FILING DATE: 19-OCT-1994
RHIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
FILING DATE: 19-OCT-1994
FILING DATE: 19-OCT-1994
FILING DATE: 19-SEP-1994
FILING DATE: 19-SEP-1994
FILING DATE: 26-APR-1994
FILING DATE: 26-APR-1994
FILING DATE: 26-APR-1994
FILING DATE: 26-APR-1994
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: Patentin Release #1
                   APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 51.
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4601 GCGGCC 4606
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCGGCC 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-611-451-51
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                                                                     0; Gaps
Length 6166;
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: linear
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                                                                                         61 GCCGC 65
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                                                     61 GCGGC
                                                                                                                                                                      US-08-439-132-1
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                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KLAUSER, THOMAS
APPLICANT: KRAWER, JOACHIM
APPLICANT: MEYER, THOMAS F.
APPLICANT: MEYER, THOMAS F.
APPLICANT: POHLMER, JOHANNES
TITLE OF INVENTION: BACTERIA USED TO PRODUCE STABLE FUSION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.2%; Score 60.2; DB 3; Length 77; Best Local Similarity 95.4%; Pred. No. 4.9e-12; Matches 62; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                     Length 73;
                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESES: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STRET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER: LOPPY disk
COMPUTER: LIBM PC COMPATIBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: LIBM PC COMPATIBLE OF PRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,354A
FILING DATE: 23-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REBEBRICE/DOCKET NUMBER: 147-157P
TELECOMMUNICATION INFORMATION:
TELEFRAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "FRAGMENT OF PLASMID pJKL65"
US-08-666-354A-10
                                                                                                                                                                                 Score 60.2; DB 1;
Pred. No. 4.9e-12;
                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08666354A Patent No. 6040141
                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                               ch 91.2%;
1 Similarity 95.4%;
62; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 base pairs
                     73 base pairs
                 LENGTH: 73 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                  61 GCGGC 65
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                                                                                                                            ; ANTI-SENSE: NO US-07-854-845B-2
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102 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGTTTCGCTACCGTAGCGCAG 161
Gaps
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0
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APPLICANT: Wong, W. K.R.
APPLICANT: Sutherland, Margaret L.
TITLE OF INVENTION: EXCRETION OF HETEROLOGOUS PROTEINS FROM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5223407; AAYMOND W.K.;SUTHERLAND, MARGARET L. TITLE OF INVENTION: EXCRETION OF HETEROLOGOUS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,132
FILING DATE: 11-MAY-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 60.2; DB 1;
95.4%; Pred. No. 6.2e-12;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/200/ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM E.COLI
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/395,797
FILING DATE: 18-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street
CITY: Washington
                                                                                                                                                                                                      ; Sequence 1, Application US/08439132; Patent No. 5646015; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.49
Warches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 249 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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1 ATGADADAGCAGCTATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCG 60
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCE: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STARE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLING DARE:
ATTORNEY AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELEPHONE: 516,742-4343
TELEPHONE: 516,742-4346
INFORMATION FOR EQU ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
                                                                                                                                                                                                     ; Sequence 1, Application US/09160567; Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 1..548
US-09-160-567-1
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                                                                61 GCGGC 65
                                                                                                     GCCGC 65
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                                                                                                                                                                                                                                                             102 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTTCGCTACCGTAGCGCAG 161
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08828741B
Fatent No. 6043069
GENERAL INPORMATION:
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinten, David M.
APPLICANT: Tratlinten, David M.
APPLICANT: Tratlinten, BRODUCING SAME
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: United States of America
ZIP: 11530
COMPUTER REABABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BEABABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BARABLE FORM:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION: Frank S.
REGISTRATION NUMBER: 31,346
REERRENCE/DOCKET NUMBER: 10591
TELEPHONE: (516) 742-4356
TELEFRAX: 230 901 SANS UR
SEQUENCE CHARACTER.FICS:
LENGTH: 54A Pare naive
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                                                                                                                                      Query Match
91.2%; Score 60.2; DB 6; Length 249;
Best Local Similarity 95.4%; Pred. No. 6.2e-12;
Matches 62; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
91.2%; Score 60.2; DB 3; Length 548;
Best Local Similarity 95.4%; Pred. No. 7.2e-12;
Matches 62; Conservative 0; Mismatches 3; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 239,145
FILING DATE: 31-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..548
                                                                                                                                                                                                                                                                                                                                          162 GCCGC 166
                                                                                                                                                                                                                                                                                                      61 GCGGC 65
                                                                                LENGTH: 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-828-741B-1
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-828-741B-1
                                                            SEQ ID NO:1
                                                                                               5223407-1
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                                                                                   1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTCGCTACCGTAGCGCAG 60
                              Gaps
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Score 60.2; DB 4; Length 548; Pred. No. 7.2e-12;
                            3; Indels
                                                      0; Mismatches
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RESULT 12

1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTGGTTTCGCTACCGTGGCCCAG 60

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ZIP: 10017-4059
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" DISKETTE
COMPUTER: 1BM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3:
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STRANDEDNESS: single strand
                                                                                                                                                                                                    711 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 GCCGAC 177
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; IMMEDIATE SOURCE:
US-08-880-829-21
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Suess, Gabriele M.
Tarlinton, David M.
Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.2%; Score 60.2; DB 4; Length 548; 95.4%; Pred. No. 7.2e-12; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                  STATE: New York

COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/710,299
FILING DATE: 09-No. 6521741-2000
CLASSIFICATION: CURROWN:
PRIOR APPLICATION NUMBER: 08/828,741
FILING DATE: ADMINON:
MAPLICATION NUMBER: 31,346
FILING DATE: CURROWN:
MARE: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
FILING NAME: SIGILO NUMBER: 31,346
TELECOMMUNICATION INFORMATION:
TELEFAX: (316) 742-4366
TELEFAX: (316) 742-4366
TELEFAX: (316) 742-4366
TELEFAX: (316) 742-4366
TELEFAX: (310) 01 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/08880829
Patent No. 5925599
BARBAL INPORMATION:
APPLICANT: Collins, John
APPLICANT: Roettgen, Peter
TITLE OF INVENTION: A Collection of Phagemids, A
TITLE OF INVENTION: Collection of Escherichia Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COCATION: 1.548

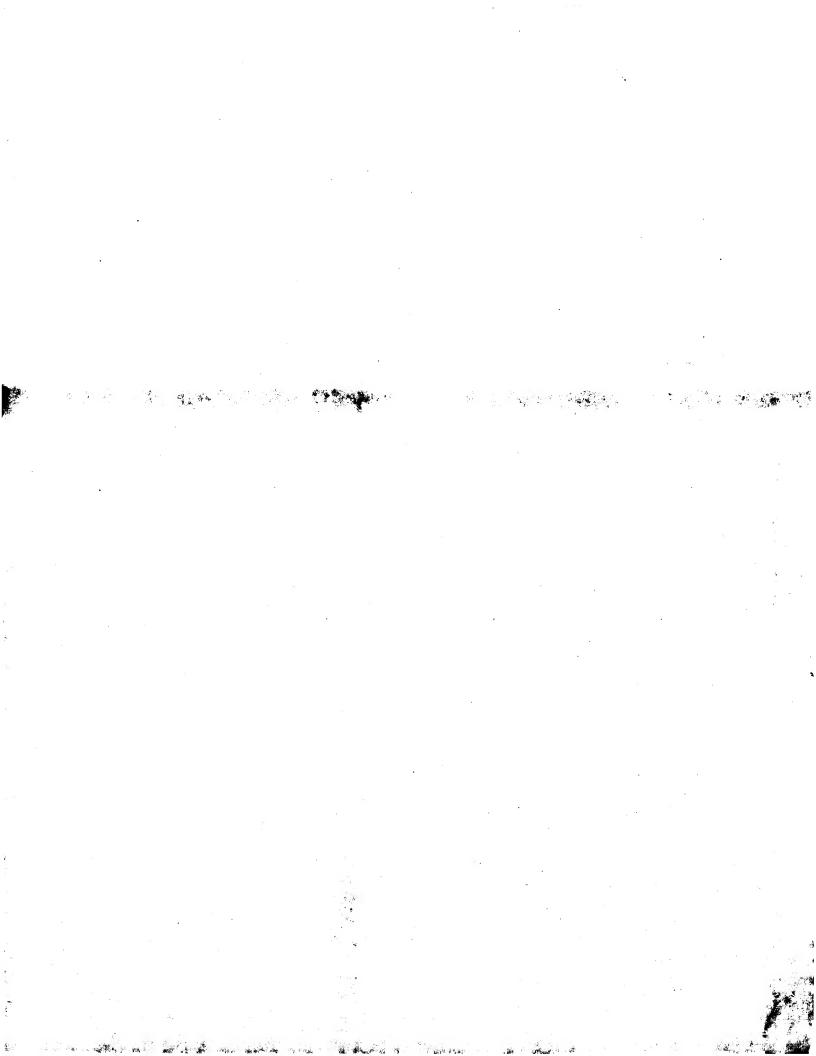
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-710-299-1
                     Sequence 1, Application US/09710299
Patent No. 6521741
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 548 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.4
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GCGGC 65
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US-09-710-299-1
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Cells Carrying The Phagemids,
Collection of Phagemid Particl
Produced From Said Collection
And Phagemid Particles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS 3.3:
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,829
FILING DATE: 23-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/458,668
FILING DATE: 06/02/95
APPLICATION NUMBER: GETMAN EP 94 108 689.4
FILING DATE: 06/07/94
ATTORNEY/AGENT INFORMATION:
NAME: EISELE, JOSEPH T:
REGISTRATION NUMBER: 25,331
REFERENCE/DOCKET NUMBER: 25,331
TELEPHONE: (212) 682-3485
TELEPHONE: GASTO ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 base pairs
TENENTH: 458 base pairs
                     TITLE OF INVENTION: COLLECTION Of Phagemid Part
TITLE OF INVENTION: Produced From Said Collect
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,
ADDRESSEE: Levy, Eisele and Richard
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Search completed: August 19, 2003, 08:35:10 Job time : 5.16534 secs
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                                              GENERAL INFORMATION:

APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tailnton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tallinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
FELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TENT: 470 base pairs
                                                                                                                                                                                                                                                                       STREET: 400 Garden City Plaza
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
Sequence 10, Application US/08828741B Patent No. 6043069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09160567
Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.3%;
Best Local Similarity 93.9%;
Matches 62; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GCGGCC 66
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US-08-828-741B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-160-567-10
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PTTCGCTACCGTGGCCCAG 60
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59.6; DB 4;
Pred. No. 1.1e-11;
0; Mismatches 4
3: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                         CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Didgiglio, Frank S.
REGISTRATION NUMBER: 31,36
REGISTRATION NUMBER: 10591
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4346
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 10:
LENGTH: 470 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.3%;
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nucleic acid
DEDNESS: single
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Best Local Similarity 93.5°
المالية المال
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
US-09-160-567-10
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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August 19, 2003, 04:46:44; Search time 18.6243 Seconds (without alignments) 7930.701 Million cell updates/sec
- nucleic search, using sw model
  OM nucleic
                                                 Run on:
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1 atgaaaaagacagctatcgc......taccgtggcccaggcggcc 66
US-09-987-455-6
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 Title:
Perfect score:
Sequence:
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apext 1.0	118970152 reg
IDENTITY NUC Gapop 10.0 , Ga	1504479 segs, 1118970152 residues
Scoring table:	Searched:

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Database :	Published_Applications_NA:*
	1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
	<pre>2: /cgnz_6/ptodata/2/pubpna/PCT NEW FUB. Beq:* 3. /cgn2_6/ptodata/2/pubpna/HSN6 NEW biff seq:*</pre>
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	6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
	7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
	8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
	9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
	<pre>10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*</pre>
	<pre>11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seg:*</pre>
	<pre>12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*</pre>
	<pre>13: /cgn2_6/ptodata/2/pubpna/US10¾_PUBCOMB.seg:*</pre>
	<pre>14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seg:*</pre>
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	<pre>16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*</pre>
	<pre>17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seg:*</pre>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1, Appli		9	2	5,	60,	Sequence 1, Appli	٦,	Sequence 10, Appl	7.	Sequence 39, Appl		15,	3,		Company 40 April
SUMMARIES		US-09-987-457-1	US-09-987-455-3	US-09-987-455-6	US-09-987-455-2	US-09-987-455-5	US-10-006-593-60	US-10-006-591-1	US-10-345-618-1	US-10-345-618-10	US-10-345-618-7	US-09-809-517A-39	US-10-345-618-5	US-10-345-618-15	US-10-345-618-3	US-09-809-517A-38	110_00_000_5178_40
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de	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.2	90.3	90.3	90.3	90.3	90.3	90.3	90.3	00
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Sequence 36, Appl Sequence 41, Appl Sequence 4, Appli Sequence 3, Appli Sequence 20, Appli Sequence 20, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 30, Appli Sequence 30, Appli Sequence 31, Appli Sequence 11, Appli	
US-10-001-934-36 US-10-001-934-36 US-09-809-517A-41 US-09-760-008A-4 US-10-076-117-3 US-09-876-494-20 US-09-916-294-4 US-09-916-20-13 US-09-916-20-13 US-09-916-20-13 US-09-916-20-13 US-09-916-20-13 US-09-916-20-13 US-09-916-20-13 US-09-912-165-19 US-09-912-165-10 US-09-912-165-10 US-09-913-1477-38 US-09-913-1477-38 US-09-913-1477-38 US-09-913-1477-38 US-09-913-1477-38 US-09-913-165-10 US-09-913-106-106-106-106-106-106-106-106-106-106	
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## ALIGNMENTS

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Sequence 1, Application US/09987457

Sequence 1, Application US/09987457

Publication No. US20030013150A1

GENERAL INFORMATION;

APPLICANT: Manosroi, Jirade;

APPLICANT: Tayapiwatana, Chatchai

APPLICANT: Tayapiwatana, Chatchai

APPLICANT: Getz, Friedrich

TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes

TITLE OF INVENTION: Methods for Large Scale Protein production in Prokaryotes

TITLE OF ILING DATE: 2001-11-14

CURRENT FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-02-1568 573

PRIOR FILING DATE: 2001-02-1568

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

LENGTH: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Escherichia coli
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Sequence 2, Application US/09987455 Publication No. US20030049729A1
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Publication No. US20030049729A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 66; Conserv
                                           61 GCGGCC 66
                                                                                    61 GCGGCC 66
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APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friaderich Geerz
APPLICANT: Friaderich Geerz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-02-15
PRIOR PILING DATE: 2001-02-15
PRIOR PILING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARRE: Patentin Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jiradej Manoscoi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: DMA-Derived tPA or K2S Molecules
FILE REFRENCE: 0652_199001
CURRENT FILING DATE: 2001-11-14
PRIOR PRIOR APPLICATION NUMBER: 05/268,574
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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100.0%; Score 66; DB 11;
Best Local Similarity 100.0%; Pred. No. 4.6e-16;
Matches 66; Conservative 0; Mismatches 0;
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Pred. No. 4.6e-16;
; Mismatches 0;
                                  Sequence 3, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09987455
Publication No. US20030049729A1
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Best Local Similarity 100.0%; Pr
Matches 66; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; ORGANISM: Escherichia coli
US-09-987-455-3
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ORGANISM: Escherichia coli
                                                                                                      APPLICANT: Aranya Manosroi
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               US-09-987-455-3
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APPLICANT: Jiradej Manoscoi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedej Manoscoi
APPLICANT: Friedej Manoscoi
APPLICANT: Friedej Manoscoi
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 052.2190001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT PILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
SOFTWARE: PALENTING OF SEQ. ID NOS: 25
SOFTWARE: PALENTING OF SEQ. ID NOS: 25
SOFTWARE: PALENTING OF SEQ. ID NOS: 21
SEQ. ID NO 2.
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APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: MADA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT PRPLICATION NUMBER: 08/09/987,455
CURRENT FILING DATE: 2001-12-15
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGTTTCGCTACCGTGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: c; CTHER INFORMATION: sequence for OmpA-K2S fusion protein US-09-987-455-2
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APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME PILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR PILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 548
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OTHER INFORMATION: Description of Artificial Sequence:LHL nucleotide
OTHER INFORMATION: sequence
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91.2%; Score 60.2; DB 12; Length 548;
Best Local Similarity 95.4%; Pred. No. 1.4e-13;
Matches 62; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                               Length 6122;
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Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
               CURRENT APPLICATION NUMBER: US/10/006,591
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/251,440
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
LENGTH: 6122
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; Sequence 10, Application US/10345618
; Publication No. US20030148484A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10345618
Publication No. US20030148484A1
GENERAL INFORMATION:
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                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 66; Conservative
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        FILE REFERENCE: 1087-3
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Publication No. US20030049731A1
Publication No. US20030049731A1
Publication No. US20030049731A1
SEREMAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: In, Ying-Chi
APPLICANT: Lin, Xing-Chi
APPLICANT: Wild, Mark
APPLICANT: Wild, Martha
APPLICANT: MCWHirter, John
TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GENES
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                                                                                                                                                  100.0%; Score 66; DB 11; Length 1128; 100.0%; Pred. No. 9.7e-16; tive 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 1.5e-15;
Live 0; Mismatches 0; Indels 0
                                          PEATURE:

OTHER INFORMATION: Description of Artificial Sequence: coding OTHER INFORMATION: sequence for OmpA-K2S fusion protein US-09-987-455-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Renenaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SEQ ID NOS: 118
SEQ ID NOS: 118
SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60, Application US/10006593
Publication No. US20030049683A1
GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: artificial sequence
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Best Local Similarity 100.
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Best Local Similarity
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                APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR PILING DATE: 2003-01-16
PRIOR PILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NO 10
LENGTH: 470
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APPLICANT: Tarlinton, David M.
APPLICANT: Treatliein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
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; LOCATION: (1)..(597)

; OTHER INFORMATION: Description of Artificial Sequence:LHL.seq

; OTHER INFORMATION: nucleotide sequence

US-10-345-618-7
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OTHER INFORMATION: Description of Artificial Sequence:Kappa OTHER INFORMATION: nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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Pred. No. 2.3e-13;
0; Mismatches 4;
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PRIOR FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10345618
Publication No. US200301484841
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 93.9%;
Matches 62; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
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Best Local Similarity
Matches 62; Conserv
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Pacient No. US20020034733A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
DATICLES OF INVENTION:
TITLE OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGTTTTCGCTACCGTAGCGCAG 325
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APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutiein, Herbert R.
TITLE OF INVENTON: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE OF INVENT APPLICATION NUMBER: US/10/345,618
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 1031
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OTHER INFORMATION: Description of Artificial Sequence:TLML nucleotide
OTHER INFORMATION: sequence
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Pred. No. 2.9e-13;
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Best Local Similarity
Matches 62, Conserv
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Best Local Similarity
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APPLICANT: Suess, Gabriele M.
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarilinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGTTTCGCTACCGTGGCCCAG
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APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
       0; Gaps
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OTHER INFORMATION: nucleotide sequence
US-10-345-618-15
    4; Indels
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                                               Query Match 90.3%; Score 59.6; DB 12; Best Local Similarity 93.9%; Pred. No. 3.2e-13; Matches 62; Conservative 0; Mismatches 4;
  0; Mismatches
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CURRENT FILING DATE: 2003-01-16
PRICA APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                              Sequence 15, Application US/10345618
Publication No. US20030148484A1
GENERAL INFORMATION:
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Publication No. US20030148484A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ.ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 1479
  62; Conservative
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                                                                                                                                     61 GCGGCC 66
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GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVERTION: particles via disulfide bonds
TITLE OF INVERTION: particles via disulfide bonds
TITLE OF INVERTION: particles via disulfide bonds
TITLE OF INVERTION: DATE: 2010-10-115
CURRENT APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOPTWARE: PatentIn version 3.0
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LOCATION: (1)..(1488)
OTHER INFORMATION: Description of Artificial Sequence:CATAB-TEV
OTHER INFORMATION: nucleotide sequence
                                                                                                           DB 12; Length 1490;
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                                                                                                        Score 59.6; DB 12
Pred. No. 3.2e-13;
0; Mismatches 4
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Job time : 19.6243 secs
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                                                                                                      ch 90.3%;
1 Similarity 93.9%;
62; Conservative (
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                                                                                                        Query Match
Best Local Similarity
Matches 62, Conserv
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US-10-345-618-3
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26.8 40.6 321 10 BE503913 26.8 40.6 325 9 AA398159 26.8 40.6 340 9 AA401699 26.8 40.6 409 13 BY641012 26.8 40.6 667 13 BX099539 26.8 40.6 667 13 BX099539 26.8 40.6 694 29 CNS04PHI 26.8 40.6 786 12 BI560274 26.8 40.6 871 13 BUS53590	26.6 40.3 268 28 26.6 40.3 379 9 26.6 40.3 450 10 26.6 40.3 472 28 26.6 40.3 642 12 26.6 40.3 642 12 26.6 40.3 753 14 26.6 40.3 753 14	26.6 40.3 885 13 BQ/3/041 26.6 40.3 889 14 CD101043 26.6 40.3 897 13 BQ733411 26.6 40.3 897 14 CB206009 26.6 40.3 1124 14 CB206009 26.2 39.7 271 9 AU184837 26.2 39.7 374 13 BQ094120 26.2 39.7 374 13 BQ38655	33 26 39.4 495 28 AQB33969 AQB33969 HS_5261_A 34 26 39.4 853 29 CNSO3TQE AL260159 Tetraodon C 36 26 39.4 1016 29 CNSO2MHS AL251231 Etraodon 37 26 39.4 1387 29 BZ557231 BZ55731 pacs1-60 38 25.6 38.8 291 14 H33495 BZ55731 pacs1-60 40 25.6 38.8 621 9 AL966295 CA377775 656425 NC 41 25.6 38.8 621 9 AL966295 AL966295 AL966295 C 34 25.6 38.8 673 9 AL64617 AL644617 AL655729 AL655729 AL655729 C 44 25.6 38.8 687 14 CA359617 AL64517 AL655729 AL630991 AL630991	ALIGNMENTS	RESULT 1 AF075794/C LOCUS LOCUS AF075794 Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium genomic clone 107-T3, genomic survey sequence. ACCESSION AF075794 AF075794. GI:3320664 SSS. SOURCE SALMONDS SALMONDS SALMONDS SALMONDELIA FREFERENCE SALMONDELIA REFERENCE TITLE SAMPLES SAMPLARS TITLE SAMPLARS TITLE COMPATION COMMENT MODELIAN MODEL	
GenCore version 5.1.6  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: August 18, 2003, 22:44:33; Search time 193.082 Seconds (without alignments)	### B307.845 Million cell updates/sec  Title:  Perfect score: 66  Sequence:  1 atgaaaaagacagctatcgcctaccgtggcccaggcggcc 66  Scoring table: IDENTITY NUC  Gapop 10.0 , Gapext 1.0	mber of hits satisfying chosen parameters:  Bs seq length: 0  Cessing: Minimum Match 0\$  Maximum Match 100\$  Listing first 45 summaries	Database: EST:*  1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estmu:* 5: em_estpl:* 7: em_estro:* 8: em_htc:* 9: 9D_est1:* 11: 9D_est2:* 12: ch_est2:*	8,8,8,8	16: em_estom:* 17: em_gss_hum:* 18: em_gss_hum:* 19: em_gss_hum:* 20: em_gss_vrt:* 21: em_gss_fun:* 22: em_gss_rum:* 23: em_gss_mam:* 24: em_gss_rum:* 25: em_gss_rum:* 26: em_gss_vrl:* 26: em_gss_vrl:* 27: em_gss_vrl:* 28: gb_gss]:* 29: gb_gss]:* 20: gb_gss]:* 29: gb_gss]:* 20: gb_	C 1 48 72.7 655 28 AF075794 AF

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Homo sapiens
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Matches 40; Conserv
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="srpg2-00054-g9"
/tissue_type="peneal gland brain"
/clone_lib="srpg2 (10238)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; peneal
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Rattus norvegicus (Satus norvegicus)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muxinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 TGAAGACGGCAGCGGCGGCGGCGCGGCGGCGGCTAGGNCAGCGACGCGGCCCGG 26
           /mol_type="genomic DNA"
/strain="LT2"
/db_xref="texon:602"
/clone="107-T3"
/clone lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
                                                                                                                                                                                                                 5 AAAAGACAGCTATCGCGATTGCAGTGGCACTGGTTTTCGCTACCGTGGCCCAGGCGG
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Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
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                                                                                                                                                        Score 48; DB 28; Length 65:
Pred. No. 8.9e-06;
1; Mismatches 8; Indels
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Location/Qualifiers
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/db_xref="taxon:10116"
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Amgen EST Program.
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RESULT

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llhi.gov/bbrp/limage/limage.html
Insert Length: 383 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
ALOJDDO RNA linear EST 14-DEC-1999
te95a03.x1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2238988 3',
mRNA sequence.
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//clone=lb="Not ID-" CGAP GC6"

//note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 125,096-1238631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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wq85e09.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2478856 3',
mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 310)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH108"
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/db_xref="taxon:9606"
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Homo sapiens
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KEYWORDS
SOURCE
ORGANISM
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Consideration of the second of the second of the second of the sequencing context of the sequencing by: Washington University Genome Sequencing Center DNA Sequencing NGI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="MICT CGAP GC6"
/note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI 'GGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1288631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 312)

                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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                                                                                                                                                                                                                                                         R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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Pred. No. 97;
0; Mismatches 22; Indels
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/lab host="DH108"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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40; Conservative (
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/lab_host="DRIOB"
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/note="Vector: pT713D-pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
scircles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Patima Bonaldo. "
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216009.81 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726760
34, mRNA sequence.
                                                                                                       Sequencing Center
information can be
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 325)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,Y., Waterston,R. and Wilson,R.
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R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. conv. Ph.D. conv. Ph.D. conv. Ph.D. conv. Ph.D. conv. Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing (Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov Seq primer: -40UP from Gibco. Seq primer: -40UP from Gibco. High quality sequence stop: 313.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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Fax: 314 286 1810
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Contact: Yoshihide Hayashizaki
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l Similarity 64.5%;
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1 (bases 1 to 340)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,Y., WashU-Merck EST Project 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 392 AGE Brror: 0.00 Seq primer: -28ml3 rev2 ET from Amersham.

Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                               organism="Homo sapiens"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muse.

(Bases 1 to 409)

Nikaido, T., Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, T., Osato, M., Saito, R., Suzuki, H., Yamanaka, T., Kiyosawa, H.,

yagi, K., Tomatu, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,

Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hune, D.A.,

Godobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hune, D.A.,

Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani

J.E., Cousins, S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,

Gough, J., Grimmond, S., Gustinoich, S., Hirokawa, N., Jackson, I. J.,

Jarvis, B.D., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons

King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons

, P.A., Majott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki,

, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G.,

Ramachandran, S., Ravasi, T., Reed, D.J., Neeld, J., Reid, J.,

Ramachandran, S., Ravasi, T., Reed, D.J., Ci, D.,

M., Shimada, K., Sultana, R., Taylor, M. S., Teasdale

, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Zimmer, A.,

Arakawa, T., Fukuda, S., Hara, A., Hashizune, W., Inotanni, K., Isahii,

, Y., Lich, M., Kagawa, I., Mirazaki, T., Waki, Y., Zimmer, A.,

Arakawa, T., Fukuda, S., Hara, A., Hashizune, W., Inotann, K., Lander

, K., Shinagawa, A., Shiraki, T., Waki, X., Sasaki, D., Salaki, D.,

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNas

All Nature 420, 563-573 (2002)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 1e+02;
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(bases 1 to 667)
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                                                                                                                                          Email: genome-resegsc.riken.go.jp,
UKL:http://genome.gsc.riken.go.jp,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura, I., Arakawa,T., Kawai,J., Konno,H., Miyazaki,A.,
T., Imocani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of a noredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Laboratory for Genome Exploration Research Group, RIKEN Genomic Schances Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                 Human Genome Sequences Mamm. Genome. 12, 673.677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rappid discovery of new genes. Genome Res. 10 (10), 1617.1630 (2000)
RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with
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/clone="K430341N20"
/tissue type="visual cortex"
/clone_lb="RIKEN full-length enriched, visual cortex"
/clone_lb="RIKEN full-length enriched, visual cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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64.5%; Pred. No. 1.1e+02;
ive 0; Mismatches 22;
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strain="C57BL/6J"
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                                                                                                 Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5', mRNA sequence.
BU783334
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library. "160 c 144 g 147 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining
clone please conteact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 429.
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(http://genome.wustl.edu/est/lambda_protocol.shtml).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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Pred. No. 1.2e+
0; Mismatches
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Matches 40; Conservative
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- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIS60274 1786 bp mRNA linear EST 05-SEP-2001 60323511F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295746 5', mRNA sequence.
BIS60274
                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 ACGTKAATGGCGGCTTTTGCGAARGCTCTKACAATACAKGAAGACGGTATCGTGGCCCAG 219
                                                                                                                                              Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 786)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Michael Balkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninoi (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
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/note="Genoscope sequence ID : COBG127CB06SP1~end :
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                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free from RZPD; context RZPD; donegrzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
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Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
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                                                                                    Contact: Ina Rolfs
SEAD Doutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGD998G231928.
                                                                                                                                                                       RZPDLIB; I.M.A.G.E. CDNA Clone Collection,
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
Http://www.rzpd.de/CloneCards/G91
bin/showLib.pl.cgi/response7libNo-972
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Fax: +49 30 32639 101
www.rzpd.de
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Pred. No. 1.2e+02;
0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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Ebert, L., Heil, O., Hennig, S., Neuber
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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| Similarity 64.5%;
| 40; Conservative
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/lab host="TMAGE:5295746"
/lab host="TMAGE:5295746"
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/clone=lib="NIH_MGC_97"
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AGENCOURT_10418173 NIH_MGC_82 Homo sapiens CDNA clone IMAGE:6620518
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2870 row: I column: 22
High quality sequence stop: 454.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 871)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mgg-llnl.gov. f column: 03
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1: Sfil (ggccgctcggcc); Site 2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGAGGGGCGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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/clone_lib="Trypanosoma cruzi random genomic library"
/clone_lib="Trypanosoma cruzi random genomic library"
/clone_lib="Trypanosoma cruzi random!vector: pBs(-) (stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphoryated
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Trypanosoma; Schizotrypanum.

1 (bases 1 to 268)

Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.

A random sequencing approach for the analysis of the trypanosoma

cruzi genome: general structure, large gene and repetitive DNA

families, and gene discovery

Genome Res. 10 (12), 1996-2005 (2000)
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Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSTc07088 Trypanosoma cruzi random genomic library Trypanosoma
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/strain="CL-Brener"
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AU244728 Shibata Xenopus AEM lambda-ZAP II cDNA library Xenopus laevis cDNA clone p5e12 5', mRNA sequence.
AU244728
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Shibata, M., Itoh, M., Ohmori, S., Shinga, J. and Taira, M.
Systematic screening and expression analysis of the head organizer genes in Kenopus embryos
Dev. Biol. 239 (2), 241-256 (2001)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Masanori Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
Graduate School of Science, University of Tokyo; CREST, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Exai: m_taira@biols.u-tokyo.ac.jp,
URL:http://www.biol.s.u-tokyo.ac.jp,users/lmb/lmb-hp.html.
Location/Qualifiers
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40.3%; Score 26.6; DB 9; Length 359;
Best Local Similarity 63.1%; Pred. No. 1.2e+02;
Matches 41; Conservative 0; Mismatches 24; Indels (
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Xenopus laevis
HincII site of the vector"
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Job time : 194.082 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - Run on:	OM protein - protein search, using sw model Run on: August 8, 2003, 17:08:17; Search time 44 Seconds
	(without alignments)
	1359.998 Million cell updates/sec

2061 1 MKKTAIAIAVALAGFATVAQ......GVYTKVTNYLDWIRDNMRPG 377 US-09-987-455-8 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 Total number of hits satisfying chosen parameters:

1107863 segs, 158726573 residues

Searched:

seq length: 0 seq length: 200000000 80 Minimum | Maximum | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	OmpA-K2S fusion pr	Human tissue plasm	mt-PA6. Escherich	Sequence of coding	Delta 2-89 tissue	Non-glycosylated t	Sequence of coding	Delta 55-62 tissue	tPA024 precursor p
;	TD	AAE25034	AAW87770	AAR25190	AAP94409	AAR68851	AAR08150	AAP94416	AAR68852	AAR05489
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## ALIGNMENTS

AAE25034 standard; Protein; 377 AA. 30-OCT-2002 (first entry) OmpA-K2S fusion protein. AAE25034; RESULT 1 AAE2503 

Tissue plasminogen activator; tPA; kringle 2 serine protease; stroke; KSS; cardiac infarction; acute myocardial infarction; pulmonary embolism; artery occlusion; deep vein thrombosis; blood clotting; thrombolytic; cerebroprotective; cardiant; ompA; fusion protein.

Unidentified

WO200240650-A2.

23-MAY-2002.

07-NOV-2001; 2001WO-EP12857.

14-NOV-2000; 2000GB-0027779.

(BOEH ) BOEHRINGER INGELHEIM INT GMBH.

Manosroi A; Tayapiwatana C, Manosroi J, Werner R, Goetz F,

WPI; 2002-519376/55. N-PSDB; AAD40614.

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                                                                                                                                    The present invention relates to a method of producing extracellularly secreted, active, correctly folded, recombinant tissue plasminogen activacor (tPA), Kringle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vein thrombosis or related diseases associated with unwanted blood clotting. The present sequence is a fusion protein comprising OmpA and K2S protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKKTAIAIAVALAGFATVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIG 60
Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKTAIAIAVALAGFATVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2061; DB 23; Length 377; 100.0%; Pred. No. 1.2e-167; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue plasminogen activator-like protease; t-PALP; human; circulatory system-related disorder; blood clotting; stroke; thrombosis; peripheral arterial occlusion; pulmonary embolism; myocardiothrombosis; diagnosis; therapy.
                                                                                                   Claim 25; Page 35-36; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW87770 standard; Protein; 372 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               377 AA;
                                                               peptide.OmpA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGBEEQK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trp; operon; tPA; finger; Kringle domain; EGF; plasminogen; fibrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQXDVPGVYTKVTNYLDWIRDNMRP 372
                                                                                                                                                                                                                                                                                                                   human mRNA for tissue plasminogen activator (tPA) It shares human mRNA for tissue plasminogen activator des AAMR9769; designated tissue plasminogen activator-like protease (t-PALP). The homology between t-PALP and tPA indicates that t-PALP may be involved in the regulation of normal and abnormal clotting in e.g. stroke, deep-vein thrombosis, peripheral arterial occlusion, pulmonary embolism and myocardiothrombosis.
                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of the translation product of the
                                                                                                                                                                                                                      New tissue plasminogen activator-like protease - useful in the diagnosis and treatment of circulatory system-related disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.1%; Score 1961; DB 20; 99.7%; Pred. No. 4.2e-159; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                        Disclosure; Page 57-58; 76pp; English
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                                                                                                                                                           Ruben SM
                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                              97US-0048000.
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(first entry)
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                                                                                                                                                                                         WPI; 1999-070207/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 355; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
WO9854199-A1
                                                              27-MAY-1998;
                                                                                              28-MAY-1997;
                               03-DEC-1998
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11-DEC-1992
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                                                                                                                                                           Ebner R,
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81 CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 ACSEGNSDCYFGNGSAYRCTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 AIFAKHRKSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGKTYRVVPGEEEGK
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                                                                                                                                                                                                                                                                               Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 438;
                                                                                                                                                                                                                                                                                                                                                           New tissue plasminogen activator - comprising finger and growth factor domains lacking tPA for longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Tissue plasminogen activator; tPA; thrombolytic agent; plasminogen; vascular diseases.
                                                                                                                                                                                                                                                                               Notani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coding region of plasmid pTQkPA dalta trp. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.1%; Score 1961; DB 10; 99.7%; Pred. No. 5.1e-159; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                               Saito Y, Sasaki H, Hayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delta 2-89 tissue plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR68851 standard; protein; 439
                                                                                                                                                                                                                                               (FUJI ) FUJISAWA PHARM CO LTD
                                                                                                                                                                             87GB-0018298.
87GB-0025052.
87GB-0026683.
                                                                                                                                              88EP-0112569
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(first entry)
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Best Local Similarity 99.7
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                            WPI; 1989-040625/06.
N-PSDB; AAN91123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 AA;
                                                                                                                                                                                             26-OCT-1987;
13-NOV-1987;
                                                                                                                                              02-AUG-1988;
                                                                                                                                                                              03-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
22-NOV-1995
                                                                                                               08-FEB-1989
                                                                              EP302456-A
                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                               Niwa M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                     The sequence given is a modified tissue plasminogen activator (tPA), mt-PA6 is diglycosylated, and lacks the finger, EGF and Kringle I domains. It may be used as a thrombolytic agent. The novel tPA posseses the properties of sparing plasminogen and fibrinogen while displaying a longer in vivo half life and providing greater maintenance of coronary blood flow.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 396;
                                                                                                                                                                                                                                          New di:glycosylated tissue plasminogen activator derivs. -
thromboembolic treatment e.g. deep vein thrombosis, acute
myocardial infarction and thrombotic stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of coding region in plasmid pTQkPA delta trp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1961; DB 13;
Pred. No. 4.6e-159;
0; Mismatches 1;
                                                                                                                                                                              Smith GF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP94409 standard; protein; 438
                                                                                                                                                                                                                                                                                                          Claim 2; Page 31; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.18;
                                                                              91EP-0311894
                                                                                                            90US-0633584
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(updated)
(first entry)
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Best Local Similarity 99.7
Matches 355; Conservative
                                                                                                                                                                             Van Jackson
                                                                                                                                           (ELIL ) LILLY & CO ELI
                                                                                                                                                                                                             WPI; 1992-219148/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 AA;
                                                                            20-DEC-1991;
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03-OCT-2002
18-JUN-1990
                                            01-JUL-1992
           EP493037-A2
                                                                                                                                                                             Burck PJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEVERYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEVEXYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid residues 2-89 contain the fibronectin and EGF regions of human tPA. Deletion of these regions results in a tissue plasminogen activator with reduced affinity for liver cell membranes, the mutant protein is not cleared from the circulation as rapidly as is wild-type tPA. The specification only gives the sequence around the deletion and not the full-length sequence of "delta 2-89 tPA"; the sequence in AAR68851 has been obtained by amending a previously disclosed wild-type human tPA sequence (from DE3930099) according to
Human; des-epidermal growth factor homologous plasminogen activator; tPA; liver membrane; reduced affinity; EGF homologous; thrombosis; thrombolytic; increased half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                              /note= "amino acids 2-89 of tPA have been deleted"
                                                                                                                                                                                                                                                                                                                                                     New modified plasminogen activator cpds. - having regions removed to reduce affinity for liver membranes and increase circulation half-life.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1961; DB 16;
Pred. No. 5.2e-159;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the description given in Example 1. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                     (AMHP ) AMERICAN HOME PROD CORP
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page ?; 26pp; English.
                                                                                                                                                                                                                                                                                                   Lee SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.1%;
                                                                                                                                                                                                  88US-0150267
                                                                                                                                                                                                                            87US-0008795
88US-0150267
                                                       (engineered)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                 Kalyan NK,
                                                                                                                                                                                                                                                                                                                            WPI; 1995-043464/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 AA;
                                                                                               Misc-difference
                                                       Homo sapiens
                                                                                                                                                                                               29-JAN-1988;
                                                                                                                                        US5376547-A
                                                                                                                                                                                                                           30-JAN-1987
                                                                                                                                                                   27-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 355;
                                                                                                                                                                                                                                                                                                 Hung PP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324
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331 SGYGKHEALSPPYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVRTVCLPPADLQLPDWTECEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSM1L1GKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DACQGDSGGPLVCLNDGRWTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNWRP 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This non-glycosylated tPA deriv. lacks the finger- and EGF-domains. It has a lower clearance rate (longer half-life) than natural tPA while retaining thrombolytic activity and stimulation by fibrin. It is produced by recombinant methods and site-specific muta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with
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                                                                                                                                                              and EGF-domains
                                                                                                                                                                                                         Tissue plasminogen activator; thrombolysis; finger domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New non-glycosylated form of tissue plasminogen activator thrombolytic activity and long plasma life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.1%; Score 1961; DB 11;
99.7%; Pred. No. 5.3e-159;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rudolph R, Fischer S,
                                                                                                                                                            Non-glycosylated tPA deriv. lacking finger-
protein; 446 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; page 15; 21pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                   90EP-0110096
                                                                                                                                                                                                                                                                                                                                                                                                                                                              89DE-3923339.
89DE-3917781.
                                                                                        (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stern A, Kohnert U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-363094/49.
standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ06762
                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1989;
                                                                                        09-JAN-2003
01-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                     05-DEC-1990
                                                                                                                                                                                                                                 domain.
                                                                                                                                                                                                                                                                                                                          EP400545-A.
                                                                                                                                                                                                                                                                            Synthetic.
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AAR08150
                                           AAR08150
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164 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKRNY 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRNPDGDAKPWCHVLKORRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEBEQK 200
                       DACOGDSGGPLVCLNDGRMTLVGIISWGLGCGOKDVPGVYTKVTNYLDWIRDNNRP 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                        Human; des-epidermal growth factor homologous plasminogen activator; tPA; liver membrane; reduced affinity; EGF homologous; thrombosis; thrombolytic; increased half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid residues 55-62 fall within the EGF region of human tPA. Deletion of these residues results in a tissue plasminogen activator with reduced affinity for liver cell membranes; the mutant protein is not cleared from the circulation as rapidly as is wild-type tPA. The specification only gives the sequence around the deletion and not the full-length sequence of "delta 55-62 tPA"; the sequence in AAR68852 has been obtained by amending a previously disclosed wild-type human tPA sequence (from DE3930099) according to the description given in Example 6. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                /note= "amino acids 55-62 of tPA have been deleted"
   321 DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified plasminogen activator cpds. - having regions removed to reduce affinity for liver membranes and increase circulation half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.1%; Score 1961; DB 16; 99.7%; Pred. No. 6.3e-159; iive 0; Mismatches 1;
                                                                                                                                                                                                                                           Delta 55-62 tissue plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                      Ź
                                                                                                                      AAR68852 standard; protein; 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMHP ) AMERICAN HOME PROD CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88US-0150267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0150267
                                                                                                                                                                                        (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                             sapiens (engineered)
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                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 54..55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalyan NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-043464/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1988;
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                                                                                                                                                                                        25-MAR-2003
22-NOV-1995
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Matches 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-1994
                                                                                                                                                        AAR68852;
                                   417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIPAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEVEKYIVHKEPDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLINRTVTDNMLCAGDTRSGGPQANLH 320
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DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.1%; Score 1961; DB 10; Length 472; larity 99.7%; Pred. No. 5.6e-159; Conservative 0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                      Tissue plasminogen activator; tPA; thrombolytic agent; plasminogen; vascular diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Notani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tissue plasminogen activator - comprising finger and growth factor domains lacking longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coding region of plasmid pmTQK112. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                        coding region in plasmid pmTQk112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page -; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FUJI ) FUJISAWA PHARM CO LID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               87GB-0025052.
87GB-0026683.
                                                                                 AAP94416 standard; protein;
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(updated)
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13-NOV-1987;
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18-JUN-1990
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Matches 355;
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                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                   AAP94416;
391
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  172 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY 231
                                           CRNPDGDAKFWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
                            CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
                                                                              141 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK
                                                                                                                                                                                                                                     DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
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                                                                                                                                                                                                                                                                                                                               AAR05488 standard; protein; 527 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88JP-0314172
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                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      tPA024 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                  (updated)
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Gushima H;
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Modified-site
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18-OCT-1990
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                                                                                                            21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                           DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
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The analogue has a longer half life and may be administered at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawasaki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tissue plasminogen activator analogues -
contg. glycosylated asparagine unit for increased half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Asn linked to oligosaccharide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.1%; Score 1961; DB 11; Best Local Similarity 99.7%; Pred. No. 6.4e-159; Matches 355; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lower doses.
(Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                     AAR05489 standard; protein; 527 AA.
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(first entry)
                                                                                                                                                                                                                                                                                                                             tPA024 precursor protein.
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Gushima H;
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N-PSDB; AAQ04903.
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Modified-site
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18-OCT-1990
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              284
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an t to Kawasaki T; The tPA analogue carries an oligosaccharide side chain linked the Asn residue replacing either Tyr-67 or Ile-86. The nature of the side chain depends on the host call used.

The analogue has a longer half life and may be administered at New tissue plasminogen activator analogues -contg. glycosylated asparagine unit for increased half-life. /note="Asn linked to oligosaccharide" Kato M, Kinoshita A, (Updated on 25-MAR-2003 to correct PA field.) 527 AA; Sequence

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292 AIFAKHRASPGERFLCGGILISSCWILSAAHCPQERFPPHHLTVILGRTYRVVPGEBEQK 351
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                                                                                                                                    Length
                                                                                                                                                                   Indels
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thrombotic disorders such as myocardial infarction. The wild-type t-PA sequence was retrieved by the in (DE3930099) and "mutated" according to the claims. See also AAR13910-14.
                                                                                                                                Score 1961; DB 12;
Pred. No. 6.4e-159;
0; Mismatches 1;
                                                                   on 25-MAR-2003 to correct PA field.)
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90JP-0050428.
90JP-0206458.
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Best Local Similarity 99.7%;
Matches 355; Conservative
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                                                                                                    527 AA
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01-MAR-1990;
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                                                                                                                                                                                                                                                                                                                                                                       The t-PA has the following amino acids of the mature protein replaced: N(37) for S, S(38) for V, G(39) for V, R(40) for E, A(41) for S and Q(42) for S. The deriv', has improved persistence in the blood compared with native t-PA, while retaining the same level of thrombolytic activity. It can be used for the treatment of
                                                                                 21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                      DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQXDVPGVYTKVTNYLDWIRDNWRP 376
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                                                    Gaps
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                    Length 527;
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                 Score 1961; DB 11;
Pred. No. 6.4e-159;
0; Mismatches 1;
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                   95.1%;
99.7%;
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90JP-0050428.
90JP-0206458.
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                                 al Similarity 99.7
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Kakutani T;
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25-NOV-1991
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               Query Match
Best Local S:
Matches 355
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90EP-0312445
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Matches 355; Conservative
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                                                                                                                                                                                                                                                                                  527 AA
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25-NOV-1991
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                                                                                                Claim 6;
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                                                                                                                                                                                                                                                                                                                                      AIFAKHRRSPGERFLCGGILISSCWILSAAHCRQERFPPHHITVILGRTYRVVPGEEEQK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
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                                                                                                                                                                                                                                                                                                                                                                                                          292 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEDK 351
                       The t-PA has the following amino acids of the mature protein replaced: N(37) for S, S(38) for V, G(39) for V, R(40) for E, A(41) for F and Q(42) for S. The deriv. has improved persistence in the blood compared with native t-PA, while retaining the same level of thrombolytic activity. It can be used for the treatment of thrombotic disorders such as myocardial infarction.
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                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                             Length 527;
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                                                                                                                                                                                                                                         Indels
                                                                                                           The wild-type t-PA sequence was retrieved by the indexer (DE3930099) and "mutated" according to the claims. See also AAR13910-14.
                                                                                                                                                                                                          95.1%; Score 1961; DB 12;
99.7%; Pred. No. 6.4e-159;
ive 0; Mismatches 1;
                                                                                                                                                    (Updated on 25-MAR-2003 to correct PA field.)
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Claim 5; Page 29; 39pp; English
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90JP-0050428.
90JP-0206458.
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(first entry)
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Matches 355, Conservative
                                                                                                                                                                                  527 AA;
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01-MAR-1990;
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25-NOV-1991
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Kakutani T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK
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tissue plasminogen derivs. - having amino acid replacements increase persistence in the blood while retaining thrombolytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 527;
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99.7%; Pred. No. 6.4e-159;
iive 0; Mismatches 1;
                                                                                                                                        Page 29; 39pp; English.
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SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The t-PA has the following amino acids of the mature protein replaced: N(115) for P and one of N(37) for S, S(38) for V, G(39) for Y, R(40) for E, A(41) for S and Q(42) for S.

The deriv. has improved persistence in the blood compared with native t-PA, while retaining the same level of thrombolytic activity. It can be used for the treatment of thrombotic disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 ACSEGNSDCYFGNGSAYRGTHSLIESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The wild-type t-PA sequence was retrieved by the indexer (DE3930099) and "mutated" according to the claims.
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99.7%; Pred. No. 6.4e-159;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yajima K, Ikenaka Y,
     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              (KANF ) KANEGAFUCHI KAGAKU KOGYO KK
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                                                                                                          label= GLY,
                                    /label= ASN,
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90JP-0206458.
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                                                                       label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagaoka T,
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                                                                                      Misc-difference 39
                                                                                                                        Misc-difference 40
   Key
Misc-difference 37
                                                      Misc-difference 38
                                                                                                                                                           Misc-difference 41
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                                                                                                                                                                                                Misc-difference
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Kakutani T;
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nes 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEBEQK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY 231
                                                                                                                                                                                                                                                                             The t-PA has the following amino acids of the mature protein replaced: G(161) for R, K(162) for R and S(165) for W. The deriv. has improved persistence in the blood compared with native t-PA, while retaining the same level of thrombolytic activity. It can be used for the treatment of thrombotic disorders such as myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGOKDVFGVYTKVTNYLDWIRDNWRP
                                                                                                                                                                          'tissue plasminogen derivs. - having amino acid replacements increase persistence in the blood while retaining thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue plasminogen activator; thrombolysis; myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 527;
                                                                                       Matsumoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                     The wild-type t-PA sequence was retrieved by the indexer (DE3930099) and "mutated" according to the claims.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1961; DB 12;
Pred. No. 6.4e-159;
0; Mismatches 1;
                                                                                      Yajima K, Ikenaka Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PA field.)
                                                 (KANF ) KANEGAFUCHI KAGAKU KOGYO KK
                                                                                                                                                                                                                                              Claim 7; Page 29; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR13914 standard; Protein; 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.1%;
90JP-0050428.
90JP-0206458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 355; Conservative
                                                                                      Nagaoka T,
                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAR13910-14
                                                                                                                                       WPI; 1991-268391/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               527 AA;
01-MAR-1990;
02-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
25-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-PA deriv.
                                                                                                    Kakutani T;
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261 412 321 472

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Sequence

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Query Match Best Local (

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Matsumoto

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Indels

Length 527;

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231

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AAR13914;

AAR1391

260

- 412 SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 471

g ð q

Search completed: August 8, 2003, 17:13:51 Job time: 45 secs

us-09-987-455-8.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 8, 2003, 17:13:07 ; Search time 20 Seconds (without alignments) 797.560 Million cell updates/sec

US-09-987-455-8

Perfect score:

2061 1 MKKTAIAIAVALAGFATVAQ......GVYTKVTNYLDWIRDNMRPG 377 Sequence:

**BLOSUM62** Scoring table:

328717 segs, 42310858 residues Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

328717

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA: Database

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMAKIES		
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	
-	1961	95.1	! !	2	US-08-811-949-63	Sequence 63, Appl	
7	1961	95.1		Н	US-07-609-510B-16	**	
m	1961	95.1		Ŋ	PCT-US91-01025A-2	C	
4	1961	95.1		9	5185259-8		
ស	1961	95.1		~	US-08-811-949-43	4	
9	1961	95.1		~	US-08-560-098A-50	50,	
7	1961	95.1		~	US-08-883-795A-38	"	
ω	1961	95.1		9			
σ	1961	95.1		9	5200340-2		
10	1961	95.1		9	5344773-2	No.	
11	1958	95.0		9	5244676-5	No.	
12	1957	95.0		~	US-08-811-949-45	ice 4	
13	1957	95.0		7	US-08-811-949-49	49,	
14	1955.5			N	US-08-811-949-65	65,	
12	1954	94.8	437	7	US-08-811-949-55		
16	1953		437	~	US-08-811-949-51	51	
17	1953	94.8	527	N	US-08-811-949-39	39	
18	1951.5	94.7	378	4	US-09-553-498-10	Sequence 10, Appl	
19	1951.5		378	4	US-09-618-869-10	10	
20	1950	94.6	355	-	US-08-137-116-1	H	
21	1950		355	٦	US-08-217-618-1	ij	
22	1950	94.6	355	Н	US-08-427-640-2	'n	
23	1950	94.6	355	Н	US-08-217-617A-1	ij	
24	1950	94.6	355	Н	US-08-217-616-1		
25	1950	94.6	355	7	US-08-811-949-53	Sequence 53, Appl	
56	1950		355	ო	US-08-794-528-1	_	
27	1950	94.6	355	9	5223256-1		

Sequence 47, Appl Sequence 57, Appl	Sequence 67, Appl Sequence 6. Appli	4 n	Patent No. 5520913	Sequence 61, Appl	Sequence 1, Appli	Sequence 8, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 51, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 72, Appl	Patent No. 5200340
US-08-811-949-47 US-08-811-949-57	US-08-811-949-67 US-08-427-640-6	US-08-427-640-4	5520913-1	US-08-811-949-61	US-08-811-949-1	US-08-427-640-8	US-09-411-977-3	US-08-558-269-6	US-09-410-882-6	US-08-560-098A-51	US-09-027-337-8	US-09-644-600-8	US-08-944-483-72	5200340-6
00	7 7	п с	w	N	7	-	4	N	m	7	7	4	m	9
355	389	356	527	354	347	356	326	383	383	477	253	253	252	546
94.6	94.3	93.8	93.6	93.1	91.3	86.7	82.7	70.7	70.7	0.69	67.0	67.0	66.7	42.7
1949	1943.5	1933.5	1929	1919.5	1882.5	1787	1704	1458	1458	1423	1380	1380	1375	880.5
28	30	32 6	3.5	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HAYASHI, MASAKO
APPLICANT: HAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
STATE: VA
CORREST: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: RIGHPY WASTER
COMPUTER: IBM PC COMPATIBLE
COMPUTER: THE PC COMPATIBLE
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 18-966-0
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3000
TELEFRAME TON A13-3220
TELEFRAME TON SEQ ID NO: 63:
                 Sequence 63, Application US/08811949; Patent No. 5840533; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 472 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-811-949-63
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                           USA
US-08-811-949-63
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY 80

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Gaps . 0

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Query Match 95.1%; Score 1961; DB 2; Length 472; Best Local Similarity 99.7%; Pred. No. 8e-186; Matches 355; Conservative 0; Mismatches 1; Indels

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320
                                                                                                             SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 471
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                              352 FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                       SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH
                                                                                                                                                                       321 DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNWRP 376
                                                                                                                                                                                             21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Generatech, Inc.
TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin
TITLE OF INVENTION: Specific Properties
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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99.7%; Pred. No. 9.3e-186;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENY APPLICATION DATA:
FILING DATE: 19910214
                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9101025A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19910214
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/486,657
FILING DATE: 1 March 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 454P:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/956-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 527 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.7
Matches 355, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94080
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TELEX: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-07-609-510B-16
; Sequence 16, Application US/07609510B
; Patent No. 5326700
; GENERAL INFORMATION:
; APPLICANY: Berg et al.
; TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue Pl
; NUMBER OF SEQUENCES: 16
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                          237 AIFAKHRKSPGERFLCGGILISSCWILSAAHCFOERFPPHHLTVILGRTYRVVPGEEEOK 296
                                                                                                                                                                                                                                                            297 FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 356
                                                                                                                                                                                                                                                                                                                                             SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 416
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177 CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 236
                                                                                                                                                  AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 200
                                                                                                                                                                                                                                    FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 260
                                                                                                                                                                                                                                                                                                                     SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
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                                                                                                                                                                                                                                                                                                                                                                                                      DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
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STRET: Lilly Corporate Center
CITY: Indianapolis
STATE: Lilly Corporate Center
STATE: Lilly Corporate Center
STATE: Lilly Corporate Center
COUNTRY: U.S.A.
ZIP: 46285
COMPUTER RADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
SOFTWARE: Microsoft Word
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,510B
FILING DATE: 19901106
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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99.7%; Pred. No. 9.3e-186;
ive 0; Mismatches 1;
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 CRNPDGDAKFWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 291
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                                 SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
                                                     412 SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 471
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352 FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 411
                                                                                                                    21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
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larity 99.7%; Pred. No. 9.3e-186;
Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                     ;Patent No. 5185259
; APPLICANT: GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA,
;VEHAR, GORDON A.
TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                              ACTIVATOR

NUMBER OF SEQUENCES: 15

CURRENT APPLICATION DATA:

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 12,694

FILING DATE: 09-FEB-1987

APPLICATION NUMBER: 483,052

FILING DATE: 07-APR-1983

APPLICATION NUMBER: 399,003

FILING DATE: 14-JUL-1982

APPLICATION NUMBER: 374,860

FILING DATE: 05-MAY-1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIWA, MINEO
SAITO, YOSHIMASA
SASAKI, HITOSHI
HAYASHI, MASAKO
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Best Local Similarity
Matches 355; Conserv
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US-08-811-949-43
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APPLICANT:
APPLICANT:
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APPLICANT: KORYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
NUMBER OF SEQUENCES: 67
ADDRESSEE: DELON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
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                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATIONG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1961; DB 2;
Pred. No. 1e-185;
0; Mismatches 1;
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; Sequence 50, Application US/08560098A
Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WARRINT, Stephan
APPLICANT: HEINZEL-WIELAND, Regine
; APPLICANT: STREFENS, Gerd JOSEÉ
; STREFENS, Gerd JOSEÉ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.1%;
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TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 99.7
Matches 355; Conservative
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LENGTH: 562 amino aci
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Vectors for
 TITLE OF INVENTION: Recombinant
TITLE OF INVENTION: Vectors for
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein (tPA)
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 99.79
Matches 355, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 AIFAKHRRSPGERFLCGGILISSCWILSAAHCPQERFPPHHLIVILGRIYRVVPGEEEQK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 140
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                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRICR APPLICATION NUMBER: P4 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 Proteins having Fibrinolytic and Coagulation-inhibiting Properties
TITLE OF INVENTION: Proteins having Fibrinolytic TITLE OF INVENTION: Coagulation-inhibiting Proper NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan STREET: 1200 G Street, N.W., Suite 700
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 355; Conserv
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                                                                                                            CITY: Wash
STATE: DC
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US-08-883-795A-38
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                                                                                                                                              COUNTRY:
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267 CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 326
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DNA Molecules and Expression
Tissue Plasminogen Activator
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Pred. No. 1e-185;
0; Mismatches 1; Indels
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; APPLICANT: GORDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA,
;VEHAR, GORDON A.
TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
                                                                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
ZIP: MSH 374
ZUP: MSH 374
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILLING DATE: 27-JUM-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 781-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 361-1398
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
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446
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          327 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 386
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                                                                  FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL
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; Patent No. 5244676
; Patent No. 5244676
; Patent No. 5244676
; TOUNAY, H.ESER, WARREN, THOMAS G.; WUN, TZE-CHEIN
; TILLE OF INVENTION: MODIFIED TISSUE PLASMINOGEN ACTIVATOR
; WITH MODIFIED GLYCOSYLATION SITE
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/203,047
                                                                                                                                                                                                                                                                                                                                   PATENT NO. 5344773

PAPLICANT: WEI, CHA-MER; HSIUNG, NANCY, REDDY, VERWURI B.;
LEMONIT, JEFFREY F.; DACKOWSKI, WILLIAM, DOUGLAS, RICHARD,
COLE, EDWARD S.; PUNCELL UR., RICHARD D.; LAU, DAVID TAL-YUI
TITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN
ACTIVATOR PRODUCED BY RECOMBIANT DNA
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/782,686
FILING DATE: 01-OCT-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 656,770
FRIEND DATE: 01-OCT-1984
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Pred. No. 1e-185;
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Best Local Similarity 99.7
Matches 355; Conservative
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; PAPLICANT: FOSTER, DONALD C.;MULVIHILL, BILEEN R.;O'HARA,
;PATRICK J.;PINGEL, KURT;YOSHITAKE, SHINJI
TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
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Pred. No. 1e-185;
0; Mismatches
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Pred. No. 1e-185;
0; Mismatches 1
APPLICATION NUMBER: US/07/489,855
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12,694
FILING DATE: 09-FEB-1987
APPLICATION NUMBER: 396,003
FILING DATE: 14-JUL1982
APPLICATION NUMBER: 374,860
FILING DATE: 05-MAY-1982
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APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
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99.7%;
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Best Local Similarity 99.7%;
Matches 355; Conservative
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Matches 355; Conservative
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                                                                                                                                                                                                                                        LENGTH: 562
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Best Local 8
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; LENGTH
5185259-3
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5200340-2
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                                                                                                                                                                                                                                                                               267 CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 326
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                                                                                                                                  Gaps
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                                                                                         Score 1958; DB 6; Length 562;
Pred. No. 2e-185;
1; Mismatches 1; Indels
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APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, WASAKO
APPLICANT: HOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCES: 67
CORRESPONDENCE ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUS
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5840533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                           95.0%;
FILING DATE: 06-JUN-1988
                                                                                                          al Similarity 99.4
354; Conservative
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MEDIUM TYPE: Floppy
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                                ; LENGTH: 562
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             SEQ ID NO:5
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s gequence 49, Application US/08811949
s Patent No. 5840533
s GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKAZU
APPLICANT: APPLICANT: 1580UB PLASMINOGEN ACTIVATOR
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                              Length 355
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                           95.0%; Score 1957; DB 2; L 100.0%; Pred. No. 1.3e-185; ive 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
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IELECOMMUNICATION INFORMATION
TELEPHONE: 703-413-3000
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ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,6
LENGTH: 355 amino acids
ryPEs: amino acid
TOPOLOGY: linear
MOLECCLE TYPE: protein
US-08-811-949-45
                                                                                                                                                                        Query Match
Best Local Similarity 100.C
Matches 354; Conservative
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INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                        1: 389 amino acids
amino acid
                                                                                                                                            Query Match
Best Local Similarity 93.2
Matches 359; Conservative
       INFORMATION FOR SEQ ID NO:
                                                                                     , MOLECULE TYPE: protein US-08-811-949-65
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                                                                                                                                                                                               21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
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                                                                                                                                                              Gaps
                                                                                                                         Length 437;
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                            Indels
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P. 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65, Application US/08811949
Fatent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: HAYASHI, MASAKO
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PILING DATE: 05-MAR-1997
                                                                                                                         Score 1957; DB 2;
Pred. No. 1.8e-185;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-99
TELECOMMUNICATION:
TELEPHONE: 703-413-2220
                                                                                                                      95.0%;
al Similarity 99.4%;
354; Conservative
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECTLE TYPE: protein
US-08-811-949-49
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-811-949-65
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185 CFQERFPPHHLTVILGRTYRVVPGEBEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSS 244
                                                                                                                                                                                                                                                    65 PWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCS 124
                                                                                                                                                                                                                                                                                                                                                            172 CFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 RCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 RCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCT 304
                                                                                                                                                                                                                     PWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCS 111
                                                                                                                                                                                                                                                                                                                             TCGLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAH 171
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                                                                                                                                            Gaps
                                                        11;
Length 389;
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Patent No. 5840533

Patent No. 5840533

APPLICANT: NIWA, MINBO
APPLICANT: SALTO, YOSHINASA
APPLICANT: ARASKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, SISSUB PLASMINOGEN ACTIVATOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                             3 KTAIAIAVALAG--FATVAQ------AASEGNSDCYFGNGSAYRG
                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATE:
FILING DATE: 05-MAR-1997
Score 1955.5; DB 2;
Pred. No. 2.1e-185;
4; Mismatches 11;
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  94.9%;
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82 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INPORMATION:
TELEPHONE: 703-413-300
NPORWATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-811-949-55
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Search completed: August 8, 2003, 17:15:51 Job time : 21 secs

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August 8, 2003, 17:15:07 ; Search time 53 Seconds (without alignments) 844.763 Million cell updates/sec
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. cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
. cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
. cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*
. cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
. cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
. cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
. cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
. cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
. cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
. cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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1. /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2. /cgn2_6/ptodata/2/pubpaa/BCT_NEW_PUB.pep:*

3. /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4. /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5. /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6. /cgn2_6/ptodata/2/pubpaa/US08_PUB.pep:*

7. /cgn2_6/ptodata/2/pubpaa/US08_PUB.pep:*

8. /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9. /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451899 segs, 118759770 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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2061
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                                                                                                                                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                 OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 8, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 18, Appl	Sequence 19, Appl	-	Sequence 8, Appli	Sequence 10, Appl	11,	145,	14,	15,	15.	16,	Sequence 12, Appl
		ID	US-09-987-455-8	US-09-084-491A-3	US-10-102-704-3	US-09-987-457-18	US-09-987-455-19	US-09-969-271-7	US-10-193-656-8	US-09-987-457-10	US-09-987-455-11	US-09-974-298-145	US-09-987-457-14	US-09-987-455-15	US-09-987-457-15	US-09-987-455-16	US-09-987-457-12
		- 1	11	σ	14	11	11	6	15	11	11	10	11	11	11	11	11
		Watch Length DB	377	372	372	527	527	562	. 562	354	354	562	343	343	343	343	339
æ	Query	Match	100.0	95.1	95.1	95.1	95.1	95.1	95.1	95.0	95.0	94.7	91.0	91.0	90.5	90.5	89.8
		Score	2061	1961	1961	1961	1961	1961	1961	1957	1957	1952	1875.5	1875.5	1865.5	1865.5	1850.5
	Result	No.	1	8	Э	4	ß	9	7	æ	თ	10	11	12	13	14	15

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Gaps

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Query Match
Best Local Similarity 100.0%; Pred: No. 8.5e-193;
Matches 377; Conservative 0; Mismatches 0; Indels 0;

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TYPE: PRT (CANISM: Artificial Sequence (CANISM: Artificial Sequence (CANISM: FEATURE: (CHER INFORMATION: Description of Artificial Sequence: OmpA-K2S (CY-997-455-8)

16   1850.5   89.8   339   11   US-09-987-455-13   Sequence 13, Appl 19   182   1837   89.1   335   11   US-09-987-455-13   Sequence 13, Appl 19   182   89.1   335   11   US-09-987-455-11   Sequence 14, Appl 19   182   89.7   331   11   US-09-987-455-11   Sequence 14, Appl 22   1704   82.7   336   11   US-09-987-455-12   Sequence 15, Appl 23   1704   82.7   336   11   US-09-987-455-12   Sequence 15, Appl 24   1704   82.7   336   11   US-09-987-455-13   Sequence 15, Appl 25   171   268   11   US-09-987-455-13   Sequence 17, Appl 26   171   268   11   US-09-987-455-13   Sequence 17, Appl 27   171   268   11   US-09-987-455-13   Sequence 17, Appl 28   171   268   11   US-09-987-455-13   Sequence 17, Appl 28   171   268   11   US-09-987-455-13   Sequence 17, Appl 30   780   77.8   411   11   US-09-987-455-13   Sequence 17, Appl 30   780   77.8   411   11   US-09-987-455-18   Sequence 17, Appl 30   780   77.8   411   11   US-09-987-455-18   Sequence 17, Appl 30   780   77.8   411   11   US-09-987-455-18   Sequence 17, Appl 30   780   77.8   411   11   US-09-987-451-29   Sequence 17, Appl 30   780   77.8   77.7   77
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257 SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 316
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                                                                                                                                                                                                                                                            197 FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
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                                                                       CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
                                                                                                                                                          137 AIFAKHRKSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK
                                         CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
                                                                                                                               141 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK
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17 ACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
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                                                                                                                                                                                                                                                                                                                                                                                                                              DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence)

Sequence No. US20020164768A1

Fublication No. US20020164768A1

GENERAL INFORMATION:

APPLICANT: Moore et al.

TITLE OF INVENTION: Tissue Plasminogen Activator-Like Protein

FILE REFERENCE: PF378C1

CURRENT FILING DATE: 2002-03-22

PRIOR FILING DATE: 1998-05-27

PRIOR PLICATION NUMBER: 09/084,491

PRIOR FILING DATE: 1998-05-27

PRIOR FILING DATE: 1997-05-28

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 372
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Pred. No. 4.9e-183;
0; Mismatches 1;
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Best Local Similarity 99.7
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-10-102-704-3
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                         KVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQ 120
                                                                                   PQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPH 180
                                                                                                               PQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPH 180
                                                                                                                                                                           HLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVV 240
                                                                                                                                                                                                                                                              RIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTV 300
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APPLICANT: RUBEN, STEVEN M.
APPLICANT: EBNER, REINHARD
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR-LIKE PROTEASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTN PLATA:
APPLICATION NUMBER: US/09/084,491A
FILING DATE: 27-MAY-1998
FILING DATE: 27-MAY-1998
GIASSIFICATION HORMATION:
ATORNEY/AGENT INFORMATION:
NAWE: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF378
TELEPHONE: (301) 309-8504
TELECOMMUNICATION INFORMATION:
TELEPRAX: (301) 309-8504
INFORMATION POR SEQ ID NO: 3:
SEQUENCE CHARRATERISTICS:
LENGTH: 372 amino acids
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95.1%; Score 1961; DB 9;
Best Local Similarity 99.7%; Pred. No. 4.9e-183;
Matches 355; Conservative 0; Mismatches 1;
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CITY: ROCKVILLE
STATE: MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TKVTNYLDWIRDNMRPG 377
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STRANDEDNESS:
TOPOLOGY: line
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PRIOR APPLICATION NUMBER: GB 00.
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 527
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Best Local Similarity 99.7%;
Matches 355; Conservative
                                                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-09-987-455-19
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                                    US-09-987-457-18

Sequence 18, Application US/09987457

Publication No. US2030013150A1

GENERAL INFORMATION:
APPLICANT: Manosroi, Aranya
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Goetz, Friedrich
APPLICANT: Goetz, Friedrich
APPLICANT: Goetz, Priedrich
APPLICANT: Goetz, Priedrich
APPLICANT: Goetz, Priedrich
APPLICANT: Goetz, Priedrich
APPLICANT: Goetz, Friedrich
APPLICANT: Merner, Rolf-Guenther
CURRENT APPLICATION NUMBER: US/09/987,457
CURRENT APPLICATION NUMBER: G0/268,573
FRIOR FILING DATE: 2001-01-14

PRIOR APPLICATION NUMBER: GB 00 27 782.2

PRIOR APPLICATION NUMBER: GB 00 27 782.2

PRIOR FILING DATE: 2001-01-14

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 18
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Sequence 19, Application US/09987455

Publication No. US2030049729A1

GENERAL INFORMATION:
APPLICANT: Aranya Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Triedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT APPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-02-15
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ORGANISM: Homo sapiens (tPA)
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Matches 355; Conservative
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                                                Indels
Score 1961; DB 11;
Pred. No. 7.9e-183;
0; Mismatches 1;
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FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 260
                                                                                                                                                            387 FEVEXYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 446
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                                                                                                                                                                                                                                                                                                                                                  DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE ACCESSION NUMBER: GenBank / P00750
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(562)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/10193656; Publication No. US20030096733A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION
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Sequence 10, Application US/09987457
; Sequence 10, Application US/09987457
; Publication No. US20030013150A1
; GENERAL INFORMATION:
; APPLICANT: Manosroi, Aranya
; APPLICANT: Manosroi, Jirade;
; APPLICANT: Tayapiwatana, Chatchai
; APPLICANT: Tayapiwatana, Chatchai
; APPLICANT: Tayapiwatana, Chatchai
; APPLICANT: Merner, Rolf-Guenther
; TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
; FILE REPREBENCE: 0652.2180001
; CURRENT APPLICATION NUMBER: 105/9997,457
; CURRENT APPLICATION NUMBER: 60/268,573
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 10
; SEQ ID NO 10
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APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REPERENCE: 0652.2190010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
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Best Local Similarity 100.0%; Pred. No. 1.1e-182;
Matches 354; Conservative 0; Mismatches 0;
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Publication No. US20030049729A1
GENERAL INFORMATION:
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US-09-987-457-14
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                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: K2S 174-527
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                                                                                                                                                                                                                                                                                95.0%; Score 1957; DB 11; Length 354; 100.0%; Pred. No. 1.1e-182; ive 0; Mismatches 0; Indels 0
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; OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CD1
US-09-974-298-145
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TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REPERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION WUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
WUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT FILING DATE: 2001-11-14
FRIOR APPLICATION NUMBER: 60/268,574
FRIOR APPLICATION NUMBER: 60 0027779.8
FRIOR APPLICATION NUMBER: GB 0027779.8
FRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 354
LENGTH: 354
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Patent No. US20020156263A1
GENERAL INFORMATION:
                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 354; Conservative
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ORGANISM: Homo sapiens
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US-09-974-298-145
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US-09-987-455-11
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LENGTH: 562
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21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY 80

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APPLICANT: Manosroi, Aranya
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE REPRENCE: 0652.2180001
CURRENT APPLICATION NUMBER: 08/09/987,457
CURRENT PILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-02-15
PRIOR PRIOR APPLICATION NUMBER: GB 00 27 782.2
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
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Publication No. US20030013150A1
GENERAL INFORMATION:
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Best Local Similarity 96.9
Matches 343; Conservative
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SEQ ID NO 15
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263 YGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDA 322
                            83 NPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAI 142
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APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT APPLICATION NUMBER: 105/0987,455
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 SEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCR
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OTHER INFORMATION: Description of Artificial Sequence: K2S 191-527,
OTHER INFORMATION: modified
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                                                                                                                                                                                                                              Sequence 15, Application US/09087455
; Publication No. US20030049729A1
; GENERAL INFORMATION:
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US-09-987-457-15
Sequence 15, Application US/09987457
Publication No. US20030013150A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-987-455-15
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APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Wenner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE REFERENCE: 0652.2180001
CURRENT APPLICATION NUMBER: US/09/987,457
CURRENT APPLICATION NUMBER: 60/268,573
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2000-11-14
NUMBER: OF SEQ ID NOS: 18
SOFTWARE: PATENTING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
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APPLICANT: Jiradej Manosroi

APPLICANT: Chatchai Tayapiwatana

APPLICANT: Chatchai Tayapiwatana

APPLICANT: Chatchai Tayapiwatana

APPLICANT: Friedrich Goetz

APPLICANT: Rolf-Guenther Werner

TITLE OF INVENTION: Methods for Large Scale Production of Recombinant

TITLE OF INVENTION: Methods for Large Scale Production of Recombinant

TITLE OF INVENTION: NA-Derived tPA or K2S Molecules

FILE REFERENCE: 6652.2190001

CURRENT APPLICATION NUMBER: US/09/987,455

CURRENT APPLICATION NUMBER: 60.268,574

PRIOR FILING DATE: 2001-02-15

PRIOR FILING DATE: 2001-02-15

PRIOR FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.5%; Score 1865.5; DB 11; Length 343; Best Local Similarity 96.6%; Pred. No. 9.2e-174; Matches 342; Conservative 0; Mismatches 1; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: recombinant K2S molecule (modified)
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Publication No. US20030049729A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: Manosroi, Aranya
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Getz, Friedrich
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE REFERENCE: 0652.2180001
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/268,573
PRIOR FILING DATE: 2000-10-2-15
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
THE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 NPDGDAKPWCHVL/KNRRLTWEYCDVPSSSTCGLRQYSQPQFRIKGGLFADIASHPWQAAI 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 YGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 SEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SEGNSD-----THSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCR 49
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                                                                                                                                                                                    FEATURE:
; CTHER INFORMATION: Description of Artificial Sequence: K2S 191-527,
; OTHER INFORMATION: modified
US-09-987-455-16
                                                                                                                                                                                                                                                                                                                                                                                         Score 1865.5; DB 11; Length 343;
Pred. No. 9.2e-174;
0; Mismatches 1; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

89.8%; Score 1850.5; DB 11; Length 339;
Best Local Similarity 95.8%; Pred. No. 2.6e-172;
Matches 339; Conservative 0; Mismatches 0; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:
CTHER INFORMATION: recombinant K2S molecule (modified)
US-09-987-457-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09987457
Publication No. US20030013150A1
GENERAL INFORMATION:
                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 96.6%;
Matches 342; Conservative
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ORGANISM: Artificial Seguence
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 343
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23 SEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCR 82

Gaps

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143 FAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFE 202
                                                                                                                                                                      203 VEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSG 262
                                                                                                                                                                                        166 VEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSG 225
                                                                                                                                                                                                                                                     226 YGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLINRTVTDNMLCAGDTRSGGPQANLHDA 285
                                                                                                                                                                                                                                   YGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDA 322
83 NPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAI
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completed: August 8, 2003, 17:23:42 ne : 54 secs Search cor Job time THIS PAGE BLANK (USPTO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2003, 17:12:22 ; Search time 19 Seconds (without alignments) 1908.189 Million cell updates/sec August Run on:

US-09-987-455-8 2061 1 MKKTAIALAVALAGFATVAQ......GVYTKVTNYLDWIRDNMRPG 377 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description .
-	1961	95.1	562	: :	UKHUT	t-plasminogen acti
7	1638.5	79.5	559	н	A35029	
٣	1600	77.6	559	н	A29941	
4	1451.5	70.4	394	7	JS0600	t-plasminogen acti
2	1428	69.3	477	~	JS0598	
9	1427	69.2	431	~	JS0599	
7	1423	69.0	477	Н	A34369	t-plasminogen acti
80	1389.5	67.4	477	N	JS0597	t-plasminogen acti
6	779.5	37.8	433	Н	UKWS	u-plasminogen acti
10	777	37.7	431	н	UKHU	
11	774.5	37.6	433	-	UKBAY	u-plasminogen acti
12	772.5	37.5	432	Н	S18932	u-plasminogen acti
13	769.5	37.3	442	Н	UKPG	
14	762	37.0	434	Н	A35005	u-plasminogen acti
15	745	•	433	Н	JN0560	u-plasminogen acti
16	738	35.8	655	-	A46688	hepatocyte growth
17	709.5	34.4	260	-	JC4795	plasma hyaluronan-
18	698.5	33.9	558	7	JC5878	plasma hyaluronan-
19	671.5	•	615	-	KFHU12	coagulation factor
20	670	32.5	603	~	S28941	coagulation factor
21	620.5		593	N	S45281	coagulation factor
22	0		812	-	PLMS	plasmin (EC 3.4.21
23	0	28.2	460	~	B61545	plasmin (EC 3.4.21
24	563.5	٠	810	N	B30848	plasmin (EC 3.4.21
25	561.5	٠	810	Н	PLHU	plasmin (EC 3.4.21
56	552.5	26.8	790	-	PLPG	_
27	550.5	26.7	812	٦	PLBO	plasmin (EC 3.4.21
28		26.5	810	N	146260	(EC 3.4
29	541.5	26.3	4548	-	800657	apoprotein(a) (EC

plasmin (BC 3.4.21	apolipoprotein(a)	brain-specific ser	membrane-bound arg	complement C3b/C4b	thrombin (EC 3.4.2	thrombin (BC 3.4.2	polyprotein - Afri	tissue kallikrein	thrombin (EC 3.4.2	hepatocyte growth	plasma kallikrein	acrosin (EC 3.4.21	hepatocyte growth	hepatocyte growth	coagulation factor
1545	698	759	7731	.5468	880	35827	F30337	35606	SHU	10579	)MSPL	:0172	0185	35644	KPHU1
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## ALIGNMENTS

t-plasminogen activator (BC 3.4.21.68) precursor [validated] - human

N;Alternate names: t-PA; tissue plasminogen activator
C;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text_change 08-Dec-2000
C; Accession: A94004; A23529; JT0562; A93293; S02125; A91343; A93951; A91322; A54645; I60
R;Ny, T.; Elgh, F.; Lund, B.
Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984
A; Title: The structure of the human tissue-type plasminogen activator gene: correlation
A;Reference number: A94004; MUID:84298137; PMID:6089198
A;Accession: A94004
A; Molecule type: DNA
A;Residues: 1-562 <nyt></nyt>
A; Cross-references: GB: L00141
A; Note: the codon given for residue 93 (ACC) is inconsistent with the authors' translati
R;Friezner Degen, S.J.; Rajput, B.; Reich, R.
J. Biol. Chem. 261, 6972-6985, 1986
A; Title: The human tissue plasminogen activator gene.
A;Reference number: A23529; MUID:86196143; PMID:3009482
A;Accession: A23529
3 Malamila himan 1913

hors' translati A;Residues: 1-562 <DEG>
A;Cross-references: GB:K03021; NID:g339817; PIDN:AAA98809.1; PID:g339818
R;Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.
Agric.-Biol. Chem. 55, 1225-1232, 1991
A;Title: Purification and characterization of tissue plasminogen activator secreted by h A;Reference number: JT0562; MUID:91291340; PMID:1368681

A; Wolecule type: mRNA A; Residues: 31-562 < ITTA A; Experimental source: embryonic lung fibroblast IMR-90 cells A; Experimental source: embryonic lung fibroblast IMR-90 cells A; Note: part of this sequence, including the amino end of the mature protein, was confir B; Pennica, D; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vehar, G.A.; Ward, C.A.; Bennett Nature 301, 214-221, 1983 A; Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche A; Reference number: A93293; MUID:83115262; PMID:6337343

A;Molecule type: mRNA A;Residues: 1-562 <PEN> A;Cross-references: GB:L00141 A;Experimental source: melanoma cells

Risabaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.
Motleic Acids Res. 16, 5695, 1988
A; Mitle: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe A; Reference number: S02125; MUID:88262579; PMID:3133640 A; Accession: S02125

A;Status: translation not shown A;Molecule type: mRNA A;Residues: 1-562 <8AS> A;Cross-references: EMBL:X07393; NID:g37243; PIDN:CAA30302.1; PID:g37244

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C;Comment: Cleavage by plasmin or trypsin produces two chains held together by a single C;Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. It C;Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t-plasminogen activator (EC 3.4.21.68)
C;Species: Rattus norvegicus (Norway ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.1%;
Best Local Similarity 99.7%;
Matches 355; Conservative (
                                                                                                                                                                                                                                                                                                               A;Map position: 8p12-8p12
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DNA 7, 671-677, 1988
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W. Wan Zonneverd, A.U.; Verman, H.; Fannexoek, H.

W. Reference number: A37567, MUID: 37033611; PMID: 3021732

A; Reference number: A37567, MUID: 37033611; PMID: 3021732

A; Contents: annotation; fibrin binding site

R; Verheijen, J.H.; Caspers, M.P. M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enger

E, Verheijen, J.H.; Caspers, M.P. M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enger

E, Sa25-3530, 1986

A; Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen ac

A; Reference number: A37568; MUID: 87161761; PMID: 3030730

A; Title: Isolation, identification and pharmacokinetic properties of human tissue-type plasminogen acrivator and its sylvations annotation; novel forms of expressed recombinant t-Pa

A; Contents: annotation; novel forms of expressed recombinant t-Pa

A; Contents: annotation; novel forms of expressed recombinant t-Pa

A; Contents: annotation; novel forms of expressed recombinant t-Pa

A; Contents: annotation; novel forms of expressed recombinant t-Pa

A; Contents: annotation; novel forms of expressed recombinant t-Pa

A; Reference number: A54645

A; Reference number: A54645; MUID: 86284200; PMID: 3090401

A; Accession: A54645

A; Cross-references: GB: M15518; NID: 9190031; PIDN: AAA60111.1; PID: 9190032

A; Redidues: 1-562 - HAR>

A; Redicues: 1-562 - HAR>

A; Redicues: 1-562 - HAR>

A; Rederence number: 180110; MUID: 88084470; PMID: 2824147

A; Rederence number: 180110; MUID: 88084470; PMID: 2824147

A; Redicues: 1-562 - HARP

A; Redicues: 1-562 - HA
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Afrecession: A91351; MulD:83169656; PMID:6572897

Afrecession: A93951; MulD:83169656; PMID:6316969

Afrecession: A93951; MulD:85000468; PMID:6433976

Afrecession: A93951

Africle: Tissue plasminogen activator: peptide analyses confirm an indirectly derived and differences number: A990488; MulD:85000468; PMID:6433976

Africle: Tissue plasminogen activator: peptide analyses confirm an indirectly derived and differences number: A990488; MulD:85000468; PMID:6433976

Africle: Tissue plasminogen activator: partial sequence of residues 36-562, active and Afrecence number: A99488; MulD:8500468; PMID:6438976

Africle: Differences between uterine and melanoma forms of tissue plasminogen activator:
Africle: Differences between uterine and melanoma forms of tissue plasminogen activator:
Africle: Differences between uterine and melanoma forms of tissue plasminogen activator:
Africle: A
A;Experimental source: fetal lung cells
R;Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma
FESS Lett. 189, 145-149, 1985
A;Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen
A;Reference number: A91343; MUID:85285620; PMID:3896853
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A;Residues: 33-45;311-320 <POH>
A;Experimental source: uterus the activation peptide may also occur after 38-Gln
A;Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
R;van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M11890; NID:g339837; PIDN:AAA61213.1; PID:g339839
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Residues: 1-36 <RE2>
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A; Thereons: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 510. C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat home C; Kaywords fibrinolysis; glycoprotein, hydrolase; kringle; plasma; serine proteinase C; Kaywords fibrinolysis; glycoprotein, hydrolase; kringle; plasma; serine proteinase F;1-23/Domain: signal sequence #status predicted <PRO> F;24-32/Domain: propertide #status predicted <PRO> F;24-32/Domain: propertide #status activator chain A #status experimental <ACH> F;31-19/Domain: EGF homology <EGF> F;31-19/Domain: kringle homology <ERS> F;31-256/Domain: kringle homology <FRO> F;31-526/Domain: kringle homology <FRO> F;31-526/Domain: trypsin homology <FRO> F;31-562/Pomain: trypsin homology <FRO> F;31-562/Pomain: trypsin homology <FRO> F;31-562/Pomain: trypsin homology <FRO> F;31-562/Pomain: argue stre: carbohydrate (Asn) (covalent) #status experimental F;310-311/Cleavage site: Arg-11e (plasmin, trypsin) #status experimental F;310-311/Cleavage site: His, Asp #status predicted F;357,406/Active site: His, Asp #status predicted F;513/Active site: Ser #status experimental
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R,Feng, P.; Ohlsson, M.; Ny, T.

Biol. Chem. 265, 2022-2027, 1990

A;Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec

A;Reference number: A35029; MUID:90130448; PMID:2105315
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A;Molecule type: DNA
A;Residues: 1.559 <FEN>
A;Residues: 1.559 <FEN>
A;Cross-references: GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g207431; GB:J05226
R;Ny, T.; Leonardsson, G.; Hsueh, A.J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 AIFAKHRESPGERFLCGGILISSCWILSAAHCFOERFPPHHLTVILGRTYRVVPGEEEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEBEQK
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Pred. No. 3.1e-162;
0; Mismatches 1;
A;Gene: GDB:PLAT
A;Cross-references: GDB:119496; OMIM:173370
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A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
C, Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;11-17/Domain: glgnal sequence #status predicted <8IG>F;11-17/Domain: propeptide #status predicted <8IG>F;130-559/Product: t-plasminogen activator #status predicted <AGH>F;30-759/Product: t-plasminogen activator chain A #status predicted <AGH>F;31-75/Domain: fibronectin type I repeat homology <IRI>F;38-75/Domain: kringle homology <IRI>F;313-75/Domain: kringle homology <IRI>F;313-75/Domain: kringle homology <IRI>F;313-75/Domain: kringle homology <IRI>F;313-75/Domain: trypsin homology <IRI
F;313-75/Domain: tr
                A, Accession: S48207
A, Molecule type: protein
A, Residues: 309-316 <LI2>
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A; Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activate A; Reference number: A31597; MUID:89170114; PMID:3148445
A; Recession: A31597
A; Molecule type: mRNA
A; Residues: 1-379, 'K', 381-559 < NNYT>
A; Rolecule type: mRNA
A; Residues: 1-379, 'K', 381-559 < NNYT>
A; Cosserefeences: GBM MAS67; NID:530159; PIDN:AA41812.1; PID:9530160
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 18-27 Domain: signal sequence # status predicted < NAT>
F; 30-559 / Product: t-plasminogen activator flata predicted < NAT>
F; 30-559 / Product: t-plasminogen activator chain A # status predicted < ACH>
F; 38-75 / Domain: EGF homology < KRL>
F; 38-75 / Domain: EGF homology < KRL>
F; 31-294 / Domain: Kringle homology < KRL>
F; 310-559 / Product: t-plasminogen activator chain B # status predicted < BCH>
F; 309-553 / Domain: trypsin homology < TRY>
F; 309-553 / Domain: trypsin homology < TRY>
F; 309-553 / Domain: trypsin homology < TRY>
F; 309-553 / Product: t-plasminogen activator chain B # status predicted
F; 309-553 / Product: t-plasminogen activator chain B * status predicted
F; 309-553 / Product: t-plasminogen activator chain B * status predicted
F; 309-553 / Product: trypsin homology < TRY>
F; 309-553 / Domain: trypsin homology < TRY>
F; 309-554 / Domain: trypsin homology < TRY>
F; 309-553 / Domain: trypsin
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C'species: Mus musculus (house mouse)
C'sAccession: A29941; 848205; 848206
R'Rickles, N.J.'Darrow, A.L.'Strickland, S.
J' Biol. Chem. 263, 1563-1569, 1988
A;Fitle: Molecular cloning of complementary DNA to mouse tissue plasminogen activator mR
A;Reference number: A29941; MUID:88087303; PMID:2826484
A;Accession: A29941
A;Molecule type: mRNA
A;References (B3-103520; MID:g202109; PIDN:AAA40470.1; PID:g202110
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Blochem. 224, 863-871, 1994
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Reference number: S48205
A;Molecule type: protein
A;Residues: 33-37, X',39-40 <LIJ>
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Best Local Similarity 82.59
Matches 287; Conservative
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A; Molecule type: mRNA
A; Residues: 1-394 < KRA>
C; Cross-references: Gs.; Mo3990; NID:g166078; PIDN:AAA31595.1; PID:g166079
A; Note: the authors translated the codon ATC for residue 75 as Thr
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-21/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                             204 ACPKGKSEDCYVGKGVTYRGTHSLITTSQASCLPWNSIVLMGKSYTAWRTNSQALGLARHN 263
                                                                                                                                                                                                                                                                            80 YCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQ 139
                                                                                                                                                                                                                                                                                                                                               323
                                                                                                                                                                                                                                                                                                                                                                                                                  140 AAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383
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                                                                                                                                                                                                                                                                                                               264 YCRNPDGDARPWCHVMKDRKLTWEYCDMSPCSTCGLRQYKRPQFRIKGGLYTDITSHPWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 AAIFVKNKKSPGERFLCGGVLISSCWVLSAAHCFLERFPPNHLKVVLGRTYRVVPGEEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 KFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AASEGNS-DCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANL
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F;37-394/Product: plasminogen activator gamma #status predicted <PLA>
                                                                      5
77.6%; Score 1600; DB 1; Length 559; 79.5%; Pred. No. 6.8e-131;
                                                                   37; Indels
                               ; Pred. No. 6.8e-131; 34; Mismatches 37;
                                   Best_Local Similarity 79.5%
Matches 283; Conservative
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Rikraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Donvenene 159-237, 1991
Gene 105, 229-237, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A;Reference number: JSOS97; MUID:92039036; PMID:1937019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: mRNA
A, Residues: 1-41 «KRA>
A, Residues: 1-41 (KRA>
C, Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat homology: sibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C, Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 1-21/Domain: signal sequence #status predicted <81G>
F; 2-36/Domain: propeptide #status predicted <81G>
F; 2-36/Domain: kringle homology < KRG>
F; 3-14/Domain: kringle homology < KRG>
F; 3-15/ADomain: kringle homology < KRG>
F; 3-15/ADomain: trypsin homology < KRG>
F; 3-18/ADOmain: trypsin homology < KRC>
F; 3-18/ADOMain: trypsin h
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16
                                                                                                                                                                        t-plasminogen activator (BC 3.4.21.68) beta precursor - common vampire bat NiAlternate names: tissue plasminogen activator (C. Species: Desmodus rotundus (common vampire bat) (C. Species: Desmodus rotundus (common vampire) (C. Species: 31.Mar-1992 #sequence_revision 31.Mar-1992 #text_change 16-Jul-1999)
                                             TGKQCEVDTHATCYKDQGVTYRGTWSTSESGAQCINWNSNLLTRRTYNGRRSDAITLGLG
                                                                                                                                     KHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCS--TCGLRQYSQPQFRIKGGLFADIA
                                                                                                                                                                                                                                                                                                          255 WTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHPWQAAIFAKHRRS PGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP
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TVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLG
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69.9%; Pred. No. 5.3e-116;
cive 41; Mismatches 66;
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Matches 253;
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Cippedies: Desmodius rotundus (common vampire bat)
Cipate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
CiAccession: J80598
Rixtaetscohmar, J: Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don Gene 105, 229-237, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des A;Reference number: J80597; MUID:92039036; PMID:1937019
A;Reference number: J80597; MUID:92039036; PMID:1937019
A;Residues: 1-477 <KRA>
A;Residues: GB:M63988; NID:g166074; PIDN:AAA31593.1; PID:g166075
C;Superfamily: tissue plasminogen activator; BGF homology; fibronectin type I repeat homology cipsus fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;22-36/Domain: gropopetide #status predicted <SIG>F;37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>
F;37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>
F;28-296/Domain: kringle homology <KRG>F;37-477/Product: rrypsin homology <RRO>F;37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>
F;28-296/Domain: kringle homology <RRO>F;28-206/Domain: kringle homology <RRO>F;28-206/Domain: kringle homology <ARN>F;28-471/Domain: krypsin homology <ARN>F;28-471/Domain: ggf homology <ARN>F;28-208/Domain: propedicted (ABA) (covalent) #status predicted
F;28-226/Cleavage site: His-Ser (plasmin) #status predicted
                            F;143-388/Domain: trypein homology <TRY>
F;143-388/Domain: trypein homology <TRY>
F;45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bonds:
F;142-143/Cleavage site: His-Ser (plasmin) #status predicted
F;189,238,345/Active site: His, Asp, Ser #status predicted
F;315/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
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                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                   SRCTSKFLFNKTVINNMLCAGDIRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSPOCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPS
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                              15;
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                                                                                                                                                                                                                                           394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477;
                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                       70.4%; Score 1451.5; DB 2; Length 67.6%; Pred. No. 3.5e-118; tive 42; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.3%; Score 1428; DB 2; Length ilarity 70.2%; Pred. No. 4.8e-116; Conservative 40; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :272,321,428/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 GVGCGEKDIPGVYTKVTNYLGWIRDNMRP 394
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 67.6'
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 254; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: 36597
C;Accession: 36597
C;Accession: 4.7 Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don Gene 105, 229-237, 1991
A;Attle: The plasminogen activator family from the salivary gland of the vampire bat Des A;Accession: 350597; MUID:92039036; PMID:1937019
                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA
A, Residues: 1-477 < KRA>
C, Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C, Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C, Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F, 1-21/Domain: propeptide #status predicted < PRO>
F, 37-477/Product: plasminogen activator alpha-1 #status predicted < PLA>
F, 87-120/Domain: EGF homology < GRE>
F, 87-120/Domain: EGF homology < KRG>
F, 128-209/Domain: kringle homology < TRY>
F, 128-209/Domain: kringle homology < TRY>
F, 128-209/Domain: kringle homology < TRY>
F, 128-209/Binding site: carbohydrate (Bsn) (covalent) #status predicted
F, 225-226/Cleavage site: His-Ser (plasmin) #status predicted
F, 222-226/Cleavage site: His-Ser (plasmin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 RVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OLPDWTECELSGYGKHEALSPPYSERLKBAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 RSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWI 370
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    common vampire bat

                                                                                                                                                                                         N'Alternate names: tissue plasminogen activator
C'Species: Desmodus rotundus (common vampire bat)
C'Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                u-plasminogen activator (EC 3.4.21.73) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A29420; A24615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCS--TCGLRQYSQPQFR1KGGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AGPATVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 ADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCFQESYLPDQLKVVLGRTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Indels
                                                                                                                                                                    t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.4%; Score 1389.5; DB 2; Best Local Similarity 69.2%; Pred. No. 1.1e-112; Matches 252; Conservative 37; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475
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375 RP 376
                                             477
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                                           RP-
                                             476
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                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
A34569
t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
C;Species: Megaderma lyra
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A34369
R;Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jacob
J. Biol. Chem. 264, 17947-17952, 1989
A;Title: Isolation, Characterization, and cDNA cloning of a vampire bat salivary plasmin
A;Reference number: A34369; MUID:90036867; PMID:2509450
A;Recession: A34369
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-477 cGAR>
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-477 cGAR>
A;Cross-references: GB:J05082; NID:g166080; PIDN:AAA31596.1; PID:g166081
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C;Superfamily: signal sequence #status predicted <SIG>F;22-36/Domain: signal sequence #status predicted <SIG>F;2-1/Domain: propeptide #status predicted <SIG>F;3-1/Domain: EGF homology <RRS>
F;1-21/Domain: EGF homology <RRS>
F;22-36/Domain: trypsin homology <RRS>
F;22-47//Promain: trypsin homology <RRS>
F;22-47/Domain: trypsin homology <RRS>
F;22-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F;272,70-73,21,428/Active site: His, Asp, Ser #status predicted
                                                                 309
                                                                                                                  314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9/
                                           255 WIECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGG
                                                                                                                                                                                                             PQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 70.2
1es 254; Conservative
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| RP 431
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Matches
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A;Molecule type: mRNA
A;Residues: 1.213, 71',215-431 <NAG2>
A;Gresidues: 1.213, 71',215-431 <NAG2>
A;Cross-references: GB:KO3226; NID:g340155; PIDN:AAC97138.1; PID:g340158; GB:D00244; NID.
R;Verde, P.; Stoppelli, M.P.; Galeffi, P.; Di Nocera, P.; Blasi, F.
R;Verde, P.; Stoppelli, M.P.; Galeffi, P.; Di Nocera, P.; Blasi, F.
A;Verde, D.; Sci. U.S.A. 81, 4727-4731, 1984
A;Title: Identification and primary sequence of an unspliced human urokinase poly(A) + RN;
A;Reference number: A37561; MUID:84272706; PMID:6589620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-150, W',152-213, 'I',215-385,'C',387-429,'V',431 <JAC>
A;Residues: 1-150, W',152-213,'I',215-385,'C',387-429,'V',431 <JAC>
A;Residues: 1-150, W',152-213,'I',215-385,'C',387-429,'V',431 <JAC>
A;Residues: 1-150, W',152-213,'I',215-385,'C',387-429,'V',431 <JAC>
B;Coshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki, Biochim. Biophys. Acta 1293, 83-89, 1996
A;Title: Characterization of single chain urokinase-type plasminogen activator with a no-A;Reference number: S65783; MUID:96186279; PMID:8652631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,Title: Molecular cloning, sequencing, and expression in Escherichia coli of human prep. N. Reference number: 138102; MUID: 85203359; PMID: 3888571
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A;Residues: 156-176,179-193,'T',195,'T',197-224 <SCH>
A;Residues: 156-176,179-193,'T',195,'T',197-224 <SCH>
A;Residues: 156-176,179-193,'T', Otting, F.; Frankus, E.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1043-1058, 1982
A;Title: The complete amino acid sequence of low molecular mass urokinase from human uri
A;Reference number: A37564; MUID:83055099; PMID:6754572
                                                                                                                                                                                                                                                                                                                                                                                                    two mRNAs coding for porcine
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A;Residues: 145-161 <NAG1>
A;Residues: 145-161 <NAG1>
A;Cross-references: GB:K03027; NID:g340174; PIDN:AAA61257.1; PID:g340175
R;Nagai, M.; Hiramatsu, R.; Kaneda, T.; Hayasuke, N.; Arimura, H.; Nishida, M.; Suyama,
Gene 36, 183-188, 1985
A;Title: Molecular cloning of cDNA coding for human preprourokinase.
A;Reference number: JT0102; MUID:86056954; PMID:2415429
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A;Molecule type: mRNA
A;Molecule type: MBL: D1143; NID:g1311467; PIDN:BAA01919.1; PID:g1199928
B;Gunzler, W.A.; Steffens, G.J.; Otting, F.; Kim, S.M.A.; Frankus, B.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1155-1165, 1982
A;Title: The primary structure of high molecular mass urokinase from human urine.
A;Reference number: A37562; WUID:83055084; PMID:6754569
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A; Residues: 21-177 < GUN>
N; Schaller, J.; Nick, H.; Rickli, E.E.; Gillessen, D.; Lergier, W.; Studer, R.O.
Eur. J. Blochem. 125, 251-257, 1982
A; Title: Human low-molecular-weight urinary urokinase. Partial characterization
A; Reference number: A37563; MUID:83003608; PMID:6749491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 66-431 <VER>
A;Cross-references: GB:D00244; NID:g220138
R;Jacobs, P.; Cravador, A.; Loriau, R.; Brockly, F.; Colau, B.; Chuchana,
DNA 4, 139-146, 1985
                                                                                                                                                         A;Residues: 1-431 cRIC>
A;Cross-references: GB:X02419; NID:g37601; PIDN:CAA26268.1; PID:g1834524
A;Note: the authors translated the codon ATG for residue 214 as 11e
R;Nagamine, Y.; Pearson, D.; Grattan, M.
Biochem. Biophys. Res. Commun. 13.5, 563-569, 1985
A;Title: Exon-intron boundary sliding in the generation of two mRNAs codi
A;Reference number: 152209; MUID:86050639; PMID:3933505
A;Accession: 152209
                                  promoter
                             and its
                         A,Title: The human urokinase-plasminogen activator gene A,Reference number: A00931; MUID:85215647; PMID:2987867
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A;Residues: 138-410 <STR:
R;Kentzer, E. Buko, A.; Menon, G.; Sarin, V.K.
Biochem. Biophys. Res. Commun. 171, 401-406, 1990
                                                                                                                                                     A; Molecule type: DNA
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R; Degen, S.J.F.; Heckel, J.L.; Reich, E.; Degen, J.L.
Biochemistry 26, 8270-8279, 1987
A; Titler The murine urokinase-type plasminogen activator gene.
A; Reference number: A29420; MUID:88163489; PMID:2831940
A; Rocession: A29420
A; Molecule type: DNA
A; Residues: 1-433 CDG3
A; Ribelin, D.; Vassalli, J.D.; Combepine, C.; Godeau, F.; Nagamine, Y.; Reich, E.; Kocher, Bur.
A; Reference number: A24615; MUID:85179474; PMID:2985383
A; Reference number: A24615; MUID:85179474; PMID:2985383
A; Residues: 1-433 - RBLA
A; Residues: 1-433 - CBLA
A; Residues: 1-434 - CCS
A; Residues: 1-433 - CBLA
A; Residues: 1-434 - CCS
A; Re
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C;Date: 17-Dec-1982 #sequence revision 04-Dec-1986 #text_change 15-Sep-2000
C;Accession: A00931; IS2209; JT0102; A37561; I38102; S65783; A37562; A37564; A35
R;Riccio, A.; Grimaldi, G.; Verde, P.; Sebastio, G.; Boast, S.; Blasi, F.
Nucleic Acids Res. 13, 2759-2771, 1985
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NAAlternate names: cellular plasminogen activator; urokinase; urokinase-type plasminogen
N;Contains: urokinase-type plasminogen activator chain A; urokinase-type plasminogen act
in form
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A;Title: Carbohydrate composition and presence of a fucose-protein linkage in recombinan A;Reference number: A35689; MUID:90365737; PMID:2393398
A;Rocession: A35689; MUID:90365737; PMID:2393398
A;Rocession: A35689
A;Rocession: A35689
A;Rocession: A35689
A;Rocession: A3689; MUID:90368-1064, 1990,
Biochem. Biophyse. Res. Commun. 13, 1058-1064, 1990,
A;Title: An amino-terminal fragment of urokinase isolated from a prostate cancer cell li A;Reference number: A36697; MUID:91097529; PMID:2125213
A;Rocession: A56697
A;Roleoule type: protein
A;Reference number: A36697; MUID:91097529; PMID:2125213
A;Rocession: A56697
A;Roleoule type: protein
A;Residues: 21-34 cRAB
R;Li, X.; Bokman, A.M.; Lilnas, M.; Smith, R.A.G.; Dobson, C.M.
Submitted to the Brockhaven Protein Data Bank, July 1993
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NWR, R;Li, X.; Smith, R.A.G.; Dobson, C.M.
Biochemistry 31, 9562-9571, 1992
A;Title: Sequential (1)H NNR assignments and secondary structure of the kringle domain fa;Reference number: A44375; MUID:93003110; PMID:1327118
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NNR, R;Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.; Mazar, A.P.; Olejniczak, submitted to the Brockhaven Protein Data Bank, January 1994
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NNR, R;Hansen, A.P.; Dolting, C.P.; Saunders, D.; Dobson, C.M.; Rypraggon, G.S.; Paillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.; Rypraggon, G.S.; Paillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.; Rypraggon, G.S.; Paillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.; Rypraggon, G.S.; Paillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.; Rypraggon, G.S.; Paillips, C.; Nowak, U.K.; Ponting, C.P.; Potting, C.P.; Rypraggon, G.S.; Paillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, C.P.; Rypraggon, G.S.; Paillips, C.F.; Nowak, U.K.; Ponting, C.P.; Paillips, C.F.; Nowak, U.K.; Ponting, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation; X-ray crystally
A; Contents: annotation; X-ray crystally
A; Contents: annotation; X-ray crystally
C; Comment: This enzyme is found in urine in a high molecular mass form, consisting of A
C; Comment: Urokinase-type plasminogen activator proteolytically activates plasminogen, a
C; Genetics:
A; Genetics:
A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.7%; Score 777; DB 1; 43.3%; Pred. No. 1.4e-59;
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157; Conserv
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CyAccession: S14687, 808651
R;Au, Y.P.T.; Wang, T.W.; Clowes, A.W.
Nucleic Acids Res. 18, 3411, 1990
A;Title: Nucleotide and deduced amno acid sequences of baboon urokinase-type plasminoge A;Title: Nucleotide and deduced amno acid sequences of baboon urokinase-type plasminoge A;Reference number: S14687, MUID:90287734; PMID:2113276
A;Reference number: S14687, MUID:90287734; PMID:2113276
A;Recession: S14687
A;Recession: S14687
A;Recession: S14687
A;Recession: S14687
A;Recence number: Nucleon S14687
A;Residues: 1-433 < AUV;
A;Residues: 1-433 < AUV;
A;Residues: Lays plasminogen activator; EGF homology; kringle homology; try. C;Reywords: glasminogen activator chain A #status predicted <ACH>F;1-20/Domain: signal sequence #status predicted <S1G>F;2-176/Product: plasminogen activator chain B #status predicted <BCH>F;30-61/Domain: trypsin homology <ACG>F;178-421/Domain: trypsin homology <ACG>F;178-421/Domain: trypsin homology <ACG>F;178-421/Domain: trypsin homology <ACG>F;178-421/Active site: His, Asp, Ser #status predicted
F;222,274,378/Active site: His, Asp, Ser #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  baboon urokinase-type plasminoge
                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                 GGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRD 372
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248 TQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLFSMYNDP 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  u-plasminogen activator (EC 3.4.21.73) precursor - yellow baboon
C;Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                     --PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRS
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                                                                                                                                              CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA
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370 MICAAD-----PÓWKT-DSCÓGDSGGPLVCSTQGKLTLTGIVSWGRECAMKDKPGVÝTRV 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Contents: annotation; correction to residue 241
                                                                                                                                                                                                                            u-plasminogen activator (EC 3.4.21.73) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: A00932
A,Molecule type: DNA
A,Residues: 1-724,'H', 242-442 <NAG1>
A,Experimental source: kidney cell line LLC-PK1
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HI 424
                                                       NM 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 NPGEMKFEVEQLILHEDFSDETLAFHNDIALLKIRTSTGGCAQPSRTIQTICLPPRFGDA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRS 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
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A; introns: 19/3; 31/1; 67/1; 125/2; 165/1; 238/2; 288/1; 335/1; 384/3
C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; tryy
C; Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
E; 1-20/Domain: signal sequence #status predicted <816; Rish-20/Domain: signal sequence #status predicted <816; Rish-20/Domain: signal sequence #status predicted <816; Rish-20/Domain: ESF homology <816; Rish-20/Domain: Kringle homology <816; Rish-20/Domain: kringle homology <816; Rish-20/Domain: Rish predicted <8179-153/Domain: wringle homology <816; Rish-20/Domain: Rish predicted <8179-153/Domain: Rish-20/Domain: Rish-20/Doma
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F,152/Binding site: carbohydrate (Asn) (covalent) #status predicted
F,179-310,220-236,228-299,324-393,356-372,383-411/Disulfide bonds: #status predicted
F,235,286,387/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGRIYRVVPGEEEOKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLPPVNGDAHFGASCEIVGFGKEDPSDYLYPEQLKMTVVKLVSHRECQQPHYYGSEVTTK 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A00932
R;Nagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucleic Acids Res. 12, 955-9541, 1984
A;Title: cDNA and gene nucleotide sequence of porcine plasminogen activator.
A;Reference number: A00932; MUID:85087954; PMID:6096832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998
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A;Reference number: A37566
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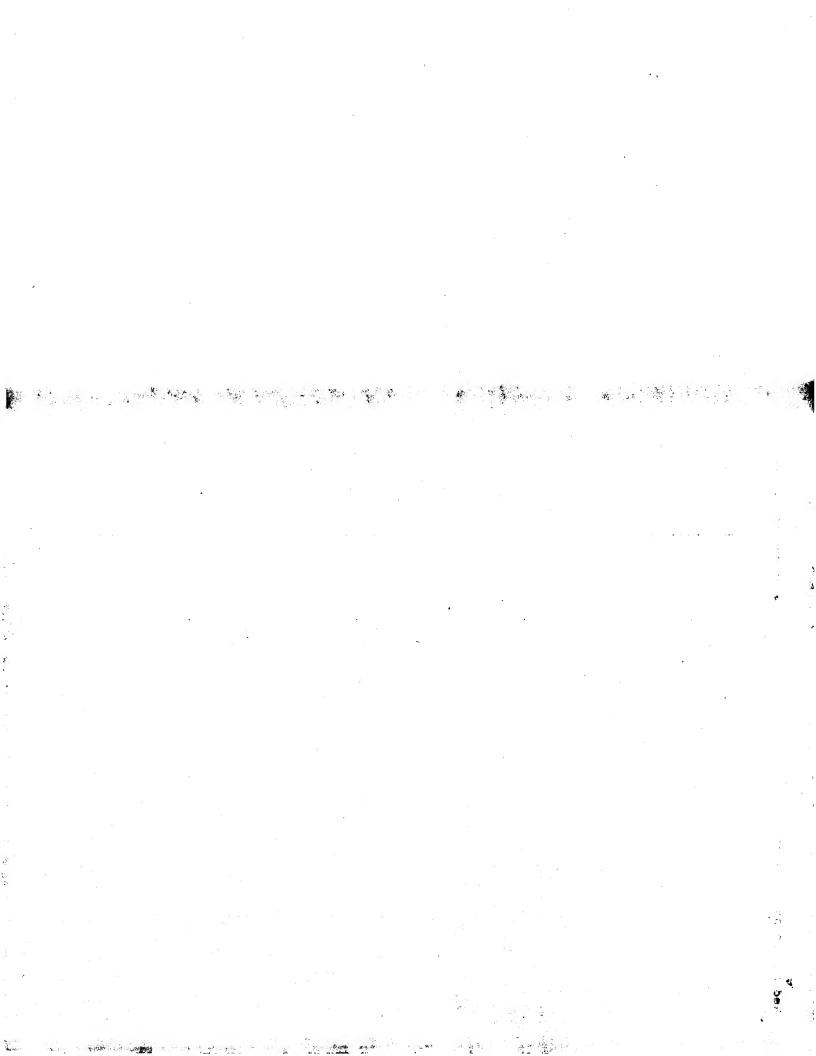
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C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
                        C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-20/Domain: signal sequence #status predicted <5IG>
F;21-179/Product: plasminogen activator chain A #status predicted <MAI>
F;21-179/Product: plasminogen activator chain A #status predicted <AGN>
F;33-64/Domain: BGF homology <BGF>
F;72-153/Domain: kringle homology <ARG>
F;181-133/Product: plasminogen activator chain B #status predicted <MA2>
F;181-421/Domain: trypsin homology <ARX>
F;181-421/Domain: trypsin homology <ARX>
F;181-421/Domain: trypsin homology <ARX>
F;170-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status predicted
F;226,277,378/Active site: His, Asp, Ser #status predicted
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                                                                                                          u-plasminogen activator (EC 3.4.21.73) precursor - chicken
N.Alternate names: upA
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Date: 20--ul-1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999
C.Accession: Ab5005
R.J.eslie, N.D.; Kessler, C.A.; Bell, S.M.; Degen, J.L.
J. Biol. Chem. 265, 1339-1344, 1990
A.Title: The chicken urokinase-type plasminogen activator gene.
A.Reference number: A35005, MUID:90110185; PMID:2295632
A.Reidues: Derliminary
A.Molecule type: mRNA
A.Residues: 1-444 cLES>
A.Reidues: 1-444 cLES
A.Re
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"Decides and activator (EC 3.4.21.73) precursor - bovine
NyAlternate names: uPA
NyAlternate names: uPA
NyAlternate names: uPA
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: JN0560
R;Kraetzschmar, J.; Heendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and inductivator and its receptor: cloning and inductivatorasion: JN0560; MUID:93216119; PMID:8385052
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A; Cross-references: GB: L03546; NID: 9163800; PIDN: AAA51419.1; PID: 9163801

A; Molecule type: mRNA A; Residues: 1-433 <KRA>

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TRGEMOFEVEKLILHEDYSAESLAHHNDIALLKIRTSRGOCAQPSRSIQTICLPPEHEDA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 --PQWET-DSCQGDSGGPLVCTIQGRLTLTGIVSWGRDCAMKYKPGVYTRVSKFLPWINT 423
                                                                                                                                         135 SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
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                                                                                                                                                                                                                        KPWCHVLKNRRLTWEYCDVPSCST------CGLRQYSQPQFRIKGGLFADIA 134
                                                                                                             29 CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA
36.1%; Score 745; DB 1; Length 433;
41.3%; Pred. No. 8.6e-57;
tive 54; Mismatches 135; Indels 24; Gaps
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Query Match 36.1%;
Best Local Similarity 41.3%;
Matches 150; Conservative 5
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HTR 426
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# 5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2003 Copyright

protein search, using sw model OM protein -

August Run on:

8, 2003, 17:10:32 ; Search time 15 Seconds (without alignments) 1181.938 Million cell updates/sec

US-09-987-455-8 2061 score: Title: Perfect g

1 MKKTAIAIAVALAGFATVAQ...........GVYTKVTNYLDWIRDNWRPG 377 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P00750 homo sapien	Q28198 bos taurus	P19637 rattus norv	P11214 mus musculu	_		P98121 desmodus ro	P98119 desmodus ro	P06869 mus musculu	P00749 homo sapien	P16227 papio cynoc	P29598 rattus norv		P15120 gallus gall		แนย ก	homo	P00748 homo sapien	cavia			P80009 canis famil	P81286 ovis aries	P12545 macaca mula	P00747 homo sapien	P06867 sus scrofa	P06868 bos taurus	-		P80010 equus cabal	_	0	O08762 mus musculu
SUMMARIES	OI.	TPA HUMAN	TPA_BOVIN	TPA_RAT	TPA_MOUSE	URTG DESRO	URT2_DESRO	URTB DESRO	URT1_DESRO	UROK_MOUSE	UROK HUMAN	UROK PAPCY	UROK RAT	UROK_PIG	UROK_CHICK	UROK_BOVIN	HGFA MOUSE	HGFA HUMAN	FA12_HUMAN	FA12_CAVPO	FA12_BOVIN	PLMN MOUSE	PLMN CANFA	PLMN_SHEEP	PLMN_MACMU	PLMN HUMAN	PLMN PIG	PLMN BOVIN	PLMN_ERIEU	APOA_HUMAN	PLMN HORSE	APOA_MACMU	NETR HUMAN	NETR_MOUSE
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## ALIGNMENTS

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SEQUENCE FROM N.A.
MEDLINE-88054470; PubMed=2824147;
Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
TISSUE=Melanoma;
MEDLINE=8115262; PubMed=6337343;
MEDLINE-8115262; PubMed=6337343;
Mard C.A., Bennett W.F., Kohr W.J., Harkins R.N., Vehar G.A.,
Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L.,
Goeddel D.V., Collen D.;
"Cloning and expression of human tissue-type plasminogen activator
CDNA in E. coli.";
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MEDLINE=88262579; PubMed=3133640;
Sasaki H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
Sasaki He, Saito You Hayashi M., Otsuka K., Niwa M.;
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Nucleic Acids Res. 16:5695-5695(1988).
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DNA 6:461-472(1987).
                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                          21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (BC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator) (Alteplase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structural domains.";
Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984)
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Friezner Degen S.J., Rajput B.;
"The human tissue plasminogen activator gene.";
J. Biol. Chem. 261:6972-6985(1986).
   562 AA.
   PRT;
TPA HUMAN STANDARD; F P00750; Q15103; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequis-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                         Nature 301:214-221(1983).
                                                                                                                          Homo sapiens (Human)
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SEQUENCE FROM N.A.
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                                                                                                                                                                      NCBI_TaxID=9606;
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SEQUENCE OF 31-562 FROM N.A.
MEDLINE-91291340; PubMed-1368681;
Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
"Purification and characterization of tissue plasminogen activator burification and characterization of Assuminogen activator burification and characterization Assuminose Secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
Agric. Biol. Chem. 55:1225-1232(1991).
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Nucleic Acids Res. 18:1086-1086(1990).
MEDLINE=86284200; PubMed=3090401;
Harris T.J., Patel T., Marston F.A., Little S., Emtage J.S.,
Opdenakker G., Volckaert G., Rombauts W., Billiau A., Somer P.;
"Cloning of cDNA coding for human tissue-type plasminogen activator
and its expression in Escherichia coli.";
Mol. Biol. Med. 3:279-292(1986).
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MEDLINE-83169656; PubMed=6572897;
Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation of cDNA sequences coding for a part of human tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-85289338; PubMed=3161893;
Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.,
Schleuning W.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                       (ISOFORM SHORT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85000468; PubMed=6433976;
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                                                                                                                                                           TISSUE=Umbilical vein;
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                                                                                                                                       FROM N.A.
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MEDLINE-90122799; PubMed=2558718;
Byeon I.-J.L., Kelley R.F., Llinas M.;
"IH NMR structural characterization of a recombinant kringle 2 domain
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MEDLINE=97449126; PubMed=9305622;
Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92106329; PubMed=1762144;
Byeon I.-J.L., Llinas M.;
"Solution structure of the tissue-type plasminogen activator kringle
2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
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EMBO J. 16:4797-4805(1997).
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                                Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H., "Purification and characterization of a melanoma cell plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91244765; PubMed=1645336; Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.; Vlahos C.J., Wilhelm of the recombinant kringle-2 domain of tissue plasminogen activator produced in Escherichia coli."; J. Biol. Chem. 266:10070-10072(1991).
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Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
MEDLINE=92118803; PubMed=1310033;
de Vos A., Ultsch M.H., Kelley R.F., Padmanabhan K., Tulinskly A.
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activator at 2.4.A resolution.";
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MEDLINE-9115408; PubMed=1900431;
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"Tissue plasminogen activator has an O-linked fucose attached to threonine-61 in the epidermal growth factor domain.";
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Biochemistry 28:9350-9360(1989).
                                                                                                                                                        J. Biochem. 132:681-686(1983)
MEDLINE=83209620; PubMed=6682760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug.";
J. Mol. Biol. 222:1035-1051(1991)
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                                                                                                                                                                                                     [14]
STRUCTURE OF CARBOHYDRATES.
                                                                                                                           activator
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EMBL outstation

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PRINTS; PR00018; KRINGLE.
                                                                                                                     EMBL; X85800; CAA59795.1; -. HSSP; P00750; 1RTF.
                                                                                                                                                                                                                                                                             Pfam; PF00008; EGF; 1.
Pfam; PF00039; fn1; 1.
Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
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566 AA;
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PROSITE; PS00021;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                      387 FEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 446
                                                                                                                                                                                                                                                                                                                                                                                        CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA 140
                                                                                                                                                                                                                          AIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQK 200
                                                                                                                                                                                                                                                                                                PEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL 260
                                                                                                                                                                                                                                                                                                                                                                      SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Int. Dairy J. 5:605-617(1995).

-1- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY CONTROLLING PLASMIN-MEDIATED PROTEDLYSIS, IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND MANY OTHER PHYSIOPATHOLOGICAL EVENTS.

-1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ravn P., Berglund L., Petersen T.E.; "Cloning and characterization of the bovine plasminogen activators uPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.
-!- PTW: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-314 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-!- MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
-!- SIMILARITY: COntains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 2 kringle domains.
                                                                                21 AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                           DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
                                                   Gaps
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SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
                                                 ö
                Length 562;
                                               1; Indels
              Score 1961; DB 1;
Pred. No. 1.1e-162;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (t-PA) (t-plasminogen activator)
              95.1%;
99.7%;
                                               Matches 355; Conservative
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                               Similarity
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AC 0281981;
DT 01-NOV-1997;
DE TISSUE-TYPE
BD (C-PA) (t-PA) (t
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). ROSITE; PS0070; KRINGLE\_1; PS0070; KRINGLE\_1; PS50240; TRYPSIN\_DOM; 1. PROSITE; PS50240; TRYPSIN\_DOM; 1. PROSITE; PS00134; TRYPSIN\_HIS; 1. PROSITE; PS00135; TRYPSIN\_BRR; 1. PROSITE; PS00135; TRYPSIN\_SRR; 1. Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Plasma; Kringle; EGF-like domain; Repeat; Signal.

21 BY SIMILARITY.

33 BY SIMILARITY.

34 SIMILARITY. KRINGLE 1.
KRINGLE 2.
SERING PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY TISSUE-TYPE PLASMINOGEN ACTIVATOR. TISSUE-TYPE PLASMINOGEN ACTIVATOR CHAIN. TISSUE-TYPE PLASMINOGEN ACTIVATOR CHAIN. FIBRONECTIN TYPE-I. EGF-LIKE. InterPro; IPR006210; IBGF. InterPro; IPR000001; Kringle. InterPro; IPR001254; Ser\_protease\_Try. FIBRONECTIN 1; 1.
KRINGLE 1; 1.
KRINGLE 2; 2. InterPro; IPR001314; Chymotrypsin. InterPro; IPR006209; EGF like. InterPro; IPR000083; Fibrnctnl. ProDom, PD000395; Kringle; 2.
SMART; SM0181; EGF; 1.
SMART; SM00181; FN1; 1.
SMART; SM00130; KR; 2.
SMART; SM0020; Tryp SPC; 1.
PROSITE; PS00126; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.

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M31190; N
M31191; N
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M31188;
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M31195;
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Peng P., Ohlsson M., Ny T.;

"The structure of the TaTA-less rat tissue-type plasminogen activator gene. Species-specific sequence divergences in the promoter predict differences in regulation of gene expression.";

"In the promoter predict of gene expression.";

"In the promoter predict convergence in regulation of gene expression.";

"In the promoter predict convergence in regulation of gene expression.";

"In the promoter predict convergence in regulation of gene expression.";

"In the promoter predict convergence in regulation of gene expression.";

"In the promoter predict convergence in regulation of practical programming of arg-|-val bond in plasmin convergence in regulation of corm plasmin convergence in the promoter predict convergence in regulation of corm plasmin convergence in the programming convergence in the programm
                                                                                 FVKNRRSPGERFLCGGILISSCWVLSAAHCFQERYPPHHLKVFLGRTYRLVPGEEEQTFE 392
                                                                                                                                                                                                                                                                                 83 NPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAI 142
                                                                                                                                                                                              FAKHRRSPGERFLCGGILISSCWILSAAHCFOERFPPHHLTVILGRTYRVVPGEEEOKFF 202
                                                                                                                                                                                                                                                           203 VEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSG 262
                                                                                                                                                                                                                                                                                                                             YCKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDA 322
                                                                 82
                                                                 23 SEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCR
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PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA. MISCELLANGOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                            376
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01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41; Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
                                                                                                                                                                                                                                                                                                                                                                                                            CQGDSGGPLVCMKDNHMTLVGIISWGLGCGRKDVPGVYTKVTNYLDMIRDNTRP
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                                   ö
80.5%; Score 1660; DB 1; Length 566; 82.8%; Pred. No. 1.5e-136; ive 24; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-89170114; PubMed-3148445;
Ny T., Leonardsson G., Hsueh A.J.W.;
NCIoning and characterization of a cDNA for rat tissue-type plasminogen activator.";
DNA 7:671-677(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559 AA
                                 293; Conservative
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                  Similarity
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Query Match
Best Local S
Matches 293
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P19637;
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DR SWART; SM00020; TR1; 1.

DR FROSITE; PS00022; EGF 1; 1.

DR FROSITE; PS00125; FIBRONECTIN 1; 1.

DR FROSITE; PS00125; FIBRONECTIN 1; 1.

DR FROSITE; PS00104; TRYPSIN DOM; 1.

DR FROSITE; PS00134; TRYPSIN DOM; 1.

DR FROSITE; PS00135; TRYPSIN HIS; 1.
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TISSUE-TYPE PLASMINOGEN ACTIVATOR
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 Egr-like domain.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 2 kringle domains.
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KRINGLE 2.
SBRINB PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; EGF_like.
InterPro; IPR00183; Fibrnctn1.
InterPro; IPR00183; Fibrnctn1.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00018; EGF; 1.
Pfam; PF00018; fn1; 1.
Pfam; PF00018; kringle; 2.
PRINTS; PR00172; CHYMOTRYPSIN.
PRINTS; PR00118; KRINGLE.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00018; KRINGLE.
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AAA42261.1; JOINED.
AAA42261.1; JOINED.
AAA42261.1; JOINED.
AAA42261.1; JOINED.
AAA4261.1; JOINED.
AAA4261.1; JOINED.
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EMBL; A31196; AAA42261.1; JK
EMBL; A19618; CAA01482.1; JR
PIR; A35029; A35029.
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AAA42261.1;
AAA42261.1;
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us-09-987-455-8.rsp

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                                                                                                                                                                                                                                     DCYVGKGVTYRGTHSFTTSKASCLPWNSMILIGKTYTAWRANSQALGLGRHNYCRNPDGD 271
                                                                                                                                                                                                                                                                                                                                                       ALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDS 327
                                                                                                                                                                                                                    DCYFGNGSAYRGTHSLTESGASCLPWNSM1L1GKVYTAQNPSAQALGLGKHNYCRNPDGD
                                                                                                                                                                                                                                                                                      RSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYI
                                                                                                                                                                                                                                                                                                                       VHKEPDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHE
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickles R.J., Darrow A.L., Strickland S.; "Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRNA and its expression during F9 teratocarcinoma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
E -> K (IN REF. 1).
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P11214; Q91VP2; D0.000-110, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2004 (Rel. 42, Last annotation update)
15-SEP-2005 (Rel. 42, Last annotation update)
15-SEP-2006 (Rel. 42, Last annotation update)
15-SEP-2007 (Rel. 42, Last annotation update)
                                                                                                                                                                                                    1;
                                                                                                                                                                                     DB 1; Length 559;
                                                                                                                                                                                                                                                                                                                                                                                       GGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNWR 375
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                                                                         BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY)
                                                                                                                                                           -> K (IN REF. 1).
7DBD3809C1D1C921 CRC64;
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Pred. No. 1.1e-134;
                                 SIMILARITY.
SIMILARITY.
SIMILARITY.
                  SIMILARITY.
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                                                           SIMILARITY
                                                                   SIMILARITY
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                                                                                                                                                                                   79.5%; Sco.
82.5%; Prective 29; I
  62903 MW;
                                                                                                                                                                                                    Matches 287; Conservative
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559 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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TISSUE-Mammary gland,

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

METARUBENER R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabs R.A.,

Rahesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FONCTION: CONVERTY THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN. TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY CONTROLLING PLASMIN-MEDIATED PROFECLYSIS, IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND MANY OTHER PHYSIOPATHOLOGICAL EVENTS.

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

-!- SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.
-!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
- PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-!- MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 2 Kringle domains.
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InterPro; IPR000083; Fibrnctnl.
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InterPro; IPR001254; Ser prot
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PRINTS; PR00018; KRINGLE.
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EMBL; BC011256; AAH11256.1;
PIR; A29941; A29941.
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SMART; SM00181; EGF; 1.
SMART; SM00058; FN1; 1.
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Pfam; PF00089; trypsin; 1.
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MGD; MGI:97610; Plat.
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                                                                  PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135, TRYPSIN HIS; 1.
PROSITE; PS00135, TRYPSIN HIS; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
Plasma; Kringle; EGF-like domain; Repeat; Signal.
                                                                                                                                          TISSUE-TYPE PLASMINOGEN ACTIVATOR.
TISSUE-TYPE PLASMINOGEN ACTIVATOR A
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                                                                                                                                                                          TISSUE-TYPE PLASMINOGEN ACTIVATOR
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N-LINKED (GLCNAC. . .)
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CHARGE RELAY SYSTEM
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34; Mismatches
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   SMART; SM00020; TTYP SPC; 1.

PROSITE; P800022; EGF 1; 1.

PROSITE; P801186; EGF 2; 1.

PROSITE; P801253; FIBRONECTIN 1; 1.

PROSITE; P850070; KRINGLE 1; 2.

PROSITE; P850070; KRINGLE 2; 2.

PROSITE; P850134; TRYPSIN HIS; 1.

PROSITE; P800134; TRYPSIN HIS; 1.
                                                                                                                       PROBABLE
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SMART; SM00130; KR; 2.
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320 HDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMR 375
                                   Donner P.; "Plasminogen activators from the saliva of Desmodus rotundus (common "Plasminogen activators from the saliva of Desmodus rotundus (common
                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403 (1992).
-!- FUNCTION: PROBABLY ESENTIAL TO SUPPORT THE FEEDING HABITS OF TH
EXCLUSIVELY HARMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Salivary gland,
MISDLINE-292039036, PubMed=1937019;
MISDLINE-292039036, PubMed=1937019;
MISDLINE-292039036, PubMed=1937019;
Alagon A., Donner P., Schleuning W.D.;
Alagon A., Donner P., Schleuning W.D.;
The plasminogen activator family from the salivary gland of the vampire bat Deemodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-1- SUBUNIT: Monomer.
-1- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
-1- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001254; Ser protease_Try.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO072; CHYMOTRYPSIN.
PRINTS; PRO018; KRINGLE.
PRODOM; PRO00195; Kringle; 1.
SMART; SM00130; KR; 1.
SMART; SM0020; Tryp SPc; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PSS0070; KRINGLE 2; 1.
PROSITE; PSS0070; TRYPSIN DOM; 1.
PROSITE; PSS00134; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P98119; 1A51.
MEROPS; S01.239; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desmodus rotundus (Vampire bat).
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                                                                                                                                                                                                                                                            STANDARD;
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CHARACTERIZATION
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                                                                                                                                                                                                                                                                             66 CINWISNLLIERTYNGRMPEAVKLGLGNHNYCRNPDGASKPWCYVIKARKFTSESCSVPV 125
                                                                                                                                                                                                                                                                                                                 CS--TCGLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWIL 167
                                                                                                                                                                                                                                                                                                                                        SAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLK 227
                                                                                                                                                                                                                                                                                                                                                                           SDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPS 287
                                                                                                                                                                                                                                                                                                                                                                                                              SRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISW 347
                                                                                                                                                                                                                                3 KTAIAIAVALAG------FATVAQAASEGNSDCYFGNGSAYRGTHSLTESGAS 49
                                                                                                                                                                                                                                           6 KTKLLCVLLCGAVFSLPRQETYRQLARGSRAYGDPHATCYKDQGVTYRGTWSTSESGAQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA alpha-2) (BAT-PA) (T-plasminogen activator)
Desmodus rotundus (Vampire bat).
                                                                                                                                                                                                                 Gaps
PROSITE; PS00135; TRYPSIN SER; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
Kringle; Signal; Multigene family.
                                   SALIVARY PLASMINOGEN ACTIVATOR GAMMA
                                                            SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
                                                                                                                                                                    LINKED (GLCNAC. . .) (POTENTIAL) 9CCD6F52F3D81FCD CRC64;
                                                                                                                                                                                                                15;
                                                                                                                                                                                              DB 1; Length 394;
                                                                                                                                                                                                                69; Indels
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(BY
                                                  SERINE PROTEASE.
CHARGE RELAY SYSTEM (I CHARGE)
BY SIMILARITY.
                                                                                                                                                                                             70.4%; Score 1451.5; DB 1, 67.6%; Pred. No. 1.3e-118; ive. 42; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 AA
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                                             KRINGLE.
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MEDLINE=92039036; PubMed=1937019;
                                                                                                                                                                             44105 MW;
                                                                                                                                                                                                                263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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142
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DISULFID
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P15638;
                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Monomer.
-!- DOMAIN: THE FIBRONECTIN TYPE-I DOMAIN MEDIATES BINDING TO FIBRIN, AND THE KRINGLE DOMAIN APPARENTLY MEDIATES FIBRIN-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity."; Ann. N.Y. Acad. Sci. 667:395-401 (1992). --i. FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE PEEDING HABITS OF THI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in plasminogen to form plasmin.
-!- ENZYME REGULATION: ACTIVITY TOWARD PLASMINOGEN IS STIMULATED IN THE PRESENCE OF FIBRIN I.
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (3)
CHARACTERIZATION.
MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                       TISSUE-Salivary gland;
MEDLINE-90016867; PubMed=2509450;
Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
Isolation, characterization, and cDNA cloning of a vampire bat salivary plasminogen activator ";
J. Biol. Chem. 264:17947-17952(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STIMULATION OF ACTIVITY.
--- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
--- SIMILARITY: Contains 1 EGF-like domain.
--- SIMILARITY: Contains 1 fibronectin type I domain.
--- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
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SWART; SW00181; EGF; 1.
SWART; SW000130; RN; 1.
SWART; SW000130; RN; 1.
SWART; SW00020; Tryp_SPC; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01253; FIBEONECTIN 1; 1.
PROSITE; PS00021; KRINGLE_1; 1.
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InterPro; IPR006209; EGF_like.
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InterPro; IPR000083; Fibrachil.
InterPro; IPR006210; IEGF.
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PRINTS; PR00018; KRINGLE.
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EMBL; J05082; AAA31596.1; -.
PIR; JS0598; JS0598.
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Pfam; PF00089; trypsin; 1.
                                                                                                                                                  Gene 105:229-237(1991)
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Pfam; PF00039; fn1; 1.
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MEROPS; S01.232; -.
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us-09-987-455-8.rsp

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01-FEB-1996 (
01-FEB-1996 (
28-FEB-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 KHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCS--TCGLRQYSQPGFRIKGGLFADIA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEEEQKFEVEKYIVHKEPDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPD 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 WIECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCTSKPLFNKTVTNNMLCAGDTRSGE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POANLHDACOGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 TVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                          SALIVARY PLASMINOGEN ACTIVATOR ALPHA FIBRONECTIN TYPE-I.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50240; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN DOW; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Plasminogen activation; Hydrolage; Serine proteage; Glycoprotein;
                                                                                                                                                          SIMILARITY).
SIMILARITY).
SIMILARITY).
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(BY
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                                                                                                                                           SERINE PROTEASE.
CHARGE RELAY SYSTEM (ECHARGE RELAY SYSTEM (ECHARGE RELAY SYSTEM (ENTERINE)
BY SIMILARITY.
                                                                    Kringle; EGF-like domain; Signal; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.3%; Score 1428; DB 1;
70.2%; Pred. No. 1.8e-116;
iive 40; Mismatches 66;
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H (IN REF. 2).
R (IN REF. 2).
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Matches 254; Conservative
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477 AA;
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STANDARD;

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ID URTB DESRO
AC P98121;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
-!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS EXCLUSIVELY HARMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Plasminogen activators from the saliva of Desmodus rotundus (common
                                                         Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
                                                                                                                                                                                                                        TISSUE-Salivary gland;
MEDLINE-292039036; PubMed=1937019;
Kraetzschmar J. Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;
The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
Kringle; EGF-like domain; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                  Petri T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SUBUNIT: Monomer.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 Kringle domain.
-!- SIMILARITY: Contains 1 BGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93393059; PubMed-1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
(Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; SO1.239; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR006209; BGF like.
InterPro; IPR006210; IBGF.
InterPro; IPR000001; Kringle.
InterPro; IPR00008; Kerypsin; PF00008; EGF; I.
Pfam; PF00008; Kringle; I.
Pfam; PF00089; trypsin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSS0240; TRYPEIN_DOM; 1.
PROSITE; PS00134; TRYPEIN HIS; 1.
PROSITE; PS00135; TRYPEIN SER; 1.
Plasminogen activation; Hydrolase;
                                                                                                Desmodus rotundus (Vampire bat).
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PRINTS; PR000139; KRINGLE.
PRODOM; PR000139; KRINGLE.
SMART; SM00181; EGF, 1.
SWART; SM00101; KR; 1.
SWART; SW001020; Tryp_SPC; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00011; KRINGLE_1; 1.
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
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CHARACTERIZATION.
                                                                                                                                                                      NCBI_TaxID=9430;
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TISSUE=Salivary gland;
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                                                                                                                                                                                                                                                                                                                                      77 KHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCS--TCGLRQYSQPQFRIKGGLFADIA 134
                                                                                                                                                                                                                                                                                                                            SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                               370 IYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGEKDIPGVYTKVTNYLGWIRDNM 429
                                                                                                                                                                                                                                                      TVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator alpha 1 precursor (BC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                      Gaps
                                SERING PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
                                            SIMILARITY).
SIMILARITY).
SIMILARITY).
          SALIVARY PLASMINOGEN ACTIVATOR BETA.
                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                  69.2%; Score 1427; DB 1; Length 431; 69.9%; Pred. No. 1.9e-116; ive 41; Mismatches 66; Indels 7
                                                                                                                                                                                         LINKED (GLCNAC. . .) (PC 699B5E675B162CBF CRC64;
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                 EGF-LIKE.
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Desmodus rotundus (Vampire bat)
                                                                                                                                                                                                 48221 MW;
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Matches 253; Conservative
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431 AA;
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P98119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: MONOMER.
-!- DOMAIN: THE FIBRONECTIN TYPE-I DOMAIN MEDIATES BINDING TO FIBRIN,
AND THE KRINGLE DOMAIN: APPARENTLY MEDIATES FIBRIN-INDUCED
STIMULATION OF ACTIVITY.
-!- SIMILARITY: ORLAINS 1 EQF-like domain.
-!- SIMILARITY: Contains 1 EQF-like domain.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity."; Ann. N.Y. Acad. Sci. 667:395-403(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. POTENT THROMBOLYTIC AGENT.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
-!- Dasminogen to form plasmin.
-!- ENZYME REGULATION: ACTIVITY TOWARD PLASMINOGEN IS STIMULATED IN
THE PRESENCE OF PIBRIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Salivary gland,
MEDLINE=98022741. PubMed=9354616;
Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,
Schleuning W.D., Bode W.;
Schleuning W.D., Bode W.;
Catalytic domain structure of vampire bat plasminogen activator:
molecular paradiam for proteolysis without activation cleavage.";
Biochemistry 36:13482-13493(1997).
-I- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE PERDING HABITS OF
MEDLINE-92039036; PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                               MEDLINE-93393059; PubMed-1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
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InterPro; IPR001001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00008; EGF; 1.
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InterPro; IPR00114; Chwotrypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR000083; Ribrnctnl.
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SMART; SM00058; FN1; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
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PRINTS; PR00018; KRINGLE.
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00181; EGF; 1.
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Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
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PDB; 1A51; 23-MAR-99.
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CHARACTERIZATION
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72

Gaps

231

190

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QLPDWTECELSGYGYGHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDT 310
                                                                                                                                                                                                                                                                                                                                                                                      311 RSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWI 370
                                                                                                                                                      113 AGY-TGKRCEVDTRATCYEGOGVTYRGTWSTAESRVECINWNSSLLTRRTYNGRMPDAFN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVKPGEEEQTFKVKKYIVHKEPDDDTYNNDIALLQLKSDSPQCAQESDSVRAICLPEANL
                                                                                                                                                                                LGLGXHNYCRNPDGDAKPWCHVLXNRRLTWEYCDVPSCS--TCGLRQYSQPQFRIKGGLF
                                                                                                                                                                                                                                             232 TDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCFQESYLPDQLKVVLGRTY
                                                                                                                                                                                                                                                                                    191 RVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADL
                                                                                                                              AGFATVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQA
                                                                                                                                                                                                                                                                                                                                                  QLPD#TECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPKFLFNKTVTNNMLCAGDT
                                                                                                                                                                                                                                 131 ADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTY
                                                                                                                                                                                                                                                                                                                                                                                                     RSGEIYPNVHDACQGDSGGFLVCMNDNHMTLLGIISWGVGCGEKDVPGVYTKVTNYLGWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus..
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=85179474; PubMed=2985383;
Belin D., Vassalli J.-D., Combepine C., Godeau F., Nagamine Y., Reich E., Kocher H.P., Duvoisin R.M.;
"Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase-type plasminogen activator.";

Eur. J. Biochem. 148:225-232(1985).
                                                                                                    3;
                                                                           Query Match 67.4%; Score 1389.5; DB 1; Length 477; Best Local Similarity 69.2%; Pred. No. 3.9e-113; ... Matches 252; Conservative 37; Mismatches 72; Indels 3;
                                                   53616 MW; AA06FD1739C10E5E CRC64;
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477 AA;
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SEQUENCE FROM N.A.
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P06869;
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                                                                                                            SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1. FIBRONECTIN TYPE-I. EGF-LIKE.
          PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50240; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_BS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PS00134; TRYPSIN_SER; 
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/FTId=CAR 000027.
N-LINKED GLCNAC. .).
/FTId=CAR 000028.
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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BY SIMILARITY.
                                                                                                                                                      KRINGLE
PS01253; FIBRONECTIN_1; 1
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365 AD----PEWKT-DSCKGDSGGPLICNIEGRPTLSGIVSWGRGCAEKNKPGVYTRVSHPL 418
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                                                                                                                                                                                                           308 GDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 367
      126 PDNOKRPWCYVQIGLRQFVQECMVHDCSLSKKPSSSVDQQGFQCG-QKALRPRFKIVGGE 184
                                                 245 KESSYNPGEMKFEVEQLILHEYYREDSLAYHNDIALLKIRTSTGQCAQPSRSIQTICLPP
                                                                                                                                                                     FADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRT
                                                                                          190 YRVVPGEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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MEDLINE=86056954; PubMed=2415429;
Nagai M., Hiramateu R., Kaneda T., Hayasuke N., Arimura H.,
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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DNA 4:139-146(1985).
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DWIQSHI 425
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
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R PRINTS; PRO0122; CHYMOTRYEIN.

R Probom; PD0001995; KRINGLE.

R SWART; SW00181; EGF; 1.

R SWART; SW00130; KR; 1.

R SWART; SW00130; KR; 1.

R PROSITE; PS00020; TGF 1; 1.

R PROSITE; PS00021; KRINGLE.

R PROSITE; PS00021; KRINGLE.

R PROSITE; PS000134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN JOM; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.
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CHAIN B (BY SIMILARITY)
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CONNECTING PEPTIDE.
SERINE PROTEASE.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. SIMILARITY: Contains 1 kringle domain. SIMILARITY: Contains 1 EGF-like domain.
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MGD, MGI:97611; Plau.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR006219; EGF like.
InterPro; IPR008010; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
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Pfam; PF00089; trypsin; 1.
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PIR; A29420; UKMS.
HSSP; P00749; 1KDU.
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

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WEDLINE=97337920; PubMed=9194591;
Warkmen B., Schmitt M., Schmalfeldt B., Trommler P., Hell W.,
Turkmen B., Schmitt M., Schmalfeldt B., Trommler P., Hell W.,
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THERAPY OF THROMBOLYTIC DISORDERS.
THERAPY OF THROMBOLYTIC DISORDERS.
C.-I- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
C.-I- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasmin B. THE HIGH MOLECULAR MASS FORM: CONSISTS
C. OF TWO CHAINA A. AND B. THE HIGH MOLECULAR MASS PORM CONTAINS A.
LONG CHAIN A. CLEAVAGE OCCURS AFTER RESIDUE 155 IN THE LOW
MOLECULAR MASS FORM TO YIELD A SHORT A1 CHAIN.
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-1- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
-1- SIMILARITY: Contains 1 Kringle domain.
-1- SIMILARITY: Contains 1 EGF-like domain.
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MEDLINE=96186279; Pubmed=8652631;
                                                                                                                                                            MEDLINE=93003110; PubMed=1327118;
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                                                                                                                                                                                                                                                                                                                         Biochemistry 31:9562-9571(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF377330; AAK53822.1; -. BC013575; AAH13575.1; -.
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                                                                                                                      STRUCTURE BY NMR OF 67-155
                                      Nature 337:579-582(1989).
dimensional NMR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activator gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARIANT LEU-141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT LEU-141.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYEGNGHFYRGKASTDTMGRSCLAWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPWCHVLKNRRLTWEYCDVPSCS------TCGLRQYSQPQFRIKGGLFADIA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50070; TRINGLE 2; 1.
PROSITE; PS50240; TRYNGLE 2; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-1ike domain; Zymogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.6%; Score 774.5; DB 1; Length 433; 43.5%; Pred. No. 9.2e-60; Live 45; Mismatches 132; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN A (BY SIMILARITY).

CHAIN B (BY SIMILARITY).

CHAIN B (BY SIMILARITY).

EGF-LIKE.

KRINGLE.

CONNECTING PEPTIDE.

SERINE PROTESE.

BY SIMILARITY.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                                                                     Interpro; IRR00001; Kringle.
InterPro; IRR00001; Kringle.
InterPro; IRR001254; Ser protease_Try.
Pfam; Pr00051; Kringle; 1.
Pfam; PR00051; CHYMOTRYPSIN.
PRINTS; PR00182; CHYMOTRYPSIN.
PRINTS; PR00181; KRINGLE.
PRODOM; PR000181; KRINGLE.
SMART; SM00130; KR; 1.
SMART; SM00120; TryP_SPC; 1.
PROSITE; PS00126; EGF 1; 1.
PROSITE; PS01186; EGF 2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                         MEROPS; S01.231; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR006209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00021; KRINGLE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48595 MW;
                                                                                                                              EMBL; X51935; CAA36200.1; -. PIR; S14687; UKBAY.
                                                                                                                                                                                                                           InterPro; IPR006210; IEGF
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                                                                                                                                                                 P00749; 1LMW.
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les 160; Conserv
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                                                                                                                                                                                                                                                              195 GEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQL 252
                                                                                                                                                                                                                                                                                                                                                                                           248 TQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                      253 PDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PQWKT-DSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRS 421
                                                                                                                                                                                                                                             -----TCGLRQYSQPQFRIKGGLFADIA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 QFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAAD--- 364
                                                                                                                                                                                                                                                                                                           SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCPQERFPPHHLTVILGRTYRVVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Thoracic aorta;
MEDLINE=90287734; PubMed=2113276;
Au Y.P.T., Wang T.W., Clowes A.W.;
"Nucleotide and deduced amino acid sequences of baboon urokinase-type
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPh)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papio cynocephalus (Yellow baboon).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
                                                                                                                                              24;
                                                                                                                 Length 431;
                                                                                                             37.7%; Score 777; DB 1; Length 43:43.3%; Pred. No. 5.6e-60; ive 48; Mismatches 134; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 AA
                                                                                                                                                                                                                                            89 KPWCHVLKNRRLTWEYCDVPSCS-----
 K03226; AAC97138.1; -
K02286; AAA61252.1; -
A21571; CAA01559.1; -
A18397; CAA01390.1; -
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                PIR; A00931; UKHU.
PDB; 1KDU; 31-OCT-93.
                                                                                                                              Similarity
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HTK 424
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                                                                                                                                              157;
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P16227;
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                                                                                                                                                           GDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbani S.A.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
--CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
--SUBMINIT: POUND IN HIGH AND LOW MOLECULAR MASS FORMS. EACH CONSISTS OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM CONTAINS A LONG CHAINS, A SUBMINIT: PASS FORM TO YIELD A SHORT AI CHAIN (BY SIMILARITY).
---SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
----SIMILARITY: Contains I EGF-like domain.
                                   247 TQGEMKFEVENLILHEDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDP
                                                                                                        AD----PQWET-DSCQGDSGGPLVCSIQGHMTLTGIVSWGRGCALKDKPGVYTRVSRFL
                195 GEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLP----P
                                                                                    248 ADLOLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 3.4.21.73) (uPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transcriptional and posttranscriptional activation of urokinase plasminogen activator gene expression in metastatic tumor cells."; Cancer Res. 52:2489-2496 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Fischer 344;
MEDLINE=2223409; PubMed=1568219;
Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,
                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
028-FEB-2003 (Rel. 41, Last annotation update)
Uroklanse-type plasminogen activator precursor (U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                            432 AA
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                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                              DWIRDNMR 375
                                                                                                                                                                                                                                                                419 PWIHSHTR 426
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InterPro; IPR006209;
InterPro; IPR006210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kefford R.F.;
                                                                                                                                                           308
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Chymotrypsin. EGF\_like. IEGF.

InterPro; IPR000001; Kringle.

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89 KPWCHVLKNRRLTWEYCDVPSCS-----TCGLRQYSQPQFRIKGGLFADIA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 NPGEMKFEVEQLILHEDFSDETLAFHNDIALLKIRTSTGGCAQPSRTIQTICLPPRFGDA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 GGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA
                                                                                                                                                                                                                PROSITE; PSS0070; KRINGLE 2; 1.
PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; FALSE NEG.
PROSITE; PS00135; TRYPSIN SER; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-like domain; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                              UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1) (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 772.5; DB 1; Length 432; 40.6%; Pred. No. 1.4e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4EB1B96C716244C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRINGLE.
CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N -> H (IN REF. 2)
E -> G (IN REF. 2)
D -> N (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERINE PROTEASE
InterPro, IPR001254; Ser_protease_Try.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-LIKE.
                                                                                               Probom; PD000395; Kringle; 1.
SMART; SM00131; EGF; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47957 MW;
                                                          PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 40.55
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 NM 374
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ACT SITE
ACT SITE
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CONFLICT
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us-09-987-455-8.rsp

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364 TNYLDWIRDNM 374
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424 SRFLTWIHTHV 434
                                                                                                                                                                          442 AA;
                                                                                                                                                                                                    Local Similarity
tes 153; Conserv
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                                                                                                                  ACT_SITE
ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
                                                                                                DISULFID
                                   DISULFID
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                         CARBOHYD
                                                                                        DISULFID
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                  DOMAIN
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UROK_CHICK
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                                                                                                                                                                               TISSUE=Kidney;
MEDLINE=65087954; PubMed=6096832;
Magamine Y., Pearson D., Altus M.S., Reich E.;
"CDNA and gene nuclectide sequence of porcine plasminogen activator.";
Nucleic Acids Res. 12:9525-9541(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-1987 (Rel. 04, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
4-EFB-2003 (Rel. 41, Last annotation update)
5-EFB-2004 (Rel. 41, Last annotation update)
6-EFB-2005 (BC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                              Nagamine Y.;
Submitted (DEC-1986) to the PIR data bank.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN A (BY SIMILARITY)
CHAIN B (BY SIMILARITY)
EGF-LIKE.
                                                                                                                                                                                                                                                                        plasminogen to form plasmin.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X01648; CAA25806.1; -. EMBL; X02724; CAA26511.1; -.
                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00749; 1KDU.
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A00932; UKPG.
                                                                                                                           Sus scrofa (Pig).
                                                                                                                                                   NCBI_TaxiD=9823;
                                                                                                                                                                                                                                      REVISION TO 241.
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HI 424
                                                 UROK PIG
P04185;
     423
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132 RPWCYVQVGLKQLVQECMVPNCSGGESHRPAYDGKNPPSTPEKVEFQCG-QKALRPRFKI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 VGGKSTTIENQPWFAAIYRRH-RGGSVTYVCGGSLISPCWVVSATHCFINYQQKEDYIVY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TCGLRQYSQPQFRI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 KGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 MLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGRIYRVVPGEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTV
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DISJ20;
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
(U-plasminogen activator).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.3%; Score 769.5; DB 1; Length 442; 41.2%; Pred. No. 2.6e-59; Live 50; Mismatches 135; Indels 33
                                                         Q -> H (IN REF. 1; CAA25806).
Q -> H (IN REF. 1; CAA26511).
A -> GS (IN REF. 1; CAA25806)
EE32PCEF501321EB CRC64;
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MEDLINE=90110185; PubMed=2295632;
Leslie N.D., Kessler C.A., Bell S.M., Degen J.L.;
"The chicken urokinase-type plasminogen activator gene.";
CONNECTING PEPTIDE SERINE PROTEASE.
                                             N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 KPWCHVLKNRRLTWEYCDVPSCS-
                                                                                                                                                                                                                                                                                                                                                                                                                      49116 MW;
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PDGDAKPWCHVLKNRRLTWEYCD-VPSCS-TCGLRQYSQPQFRIKGGLFADIASHPWQAA 141
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50U10; NATURE DOM; 1.
PROSITE; PS60240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN ER; 1.
PROSITE; PS00135; TRYPSIN ER; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-like domain; Signal; Zymogen.

20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
.) (POTENTIAL).
         -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in plasminogen to form plasmin.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 BGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 434;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.0%; Score 762; DB 1; Length 43 45.4%; Pred. No. 1.1e-58; ive 56; Mismatches 116; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN A (BY SIMILARITY)
CHAIN B (BY SIMILARITY)
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERINE PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC
                                                                                                                                                                                                  EMBL; J05188; AAA49130.1; -...
PIR; A35005; A35005.1; -...
HSSP; P00763; 1DP0.
MEROPES; S01.231; -...
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR006210; EGF like.
InterPro; IPR006210; EGF.
InterPro; IPR00001; Kringle.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00091; kringle; 1...
Pfam; PF00099; trypsin; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRINGLE
J. Biol. Chem. 265:1339-1344 (1990)
                                                                                                                                                                                                                                                                                                                                                                  Prodom; PD000335; Kringle; 1.
SMART; SM00181; EGF; 1.
SMART; SM00180; KR; 1.
SMART; SM00100; Tryp, SPC; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00021; KRINGLE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49400 MW;
                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                         EMBL; J05187; AAA49131.1; -.
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158
172
434
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379
358
397
217
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21
173
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79
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PROSITE;
PROSITE;
PROSITE;
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CARBOHYD
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26 NSDCYFGNGSAYRGTHSLTESGASCLPWN--SMILIGKVYTAQNPSAQALGLGKHNYCRN

Gaps

Conservative

163;

Best Loca Matches

Š 쉼.

96

Local Similarity

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EQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDW 255
                                                                                                                                                        248 EQVEMVDEIISHPDFTDHTGGNDNDIALIRIRTASGQCAVESNYVRTVCLPEKNINLYDN 307
                                                                                                                                                                                                               TECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGP 315
                                                                                                                                                                                                                                   142 IFAKHRRSPGERFLCGGILISSCWILSAAHCFQE--RFPPHH--LTVILGRTYRVVPGEE 197
                                                                                                                                                                                                                                                                                                                                 420
                                                                                                                                                                                                                                                                                          316 QANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Cloning and characterization of the bovine plasminogen activators uPA
                                                                                                                                                                                                                                                                                                                 363 LWET-DACKGDSGGPMVCEHNGRMTLYGIVSWGDGCAKKNKPGVYTRVTRYLNWIDSNM
                                                                                                                                                                                                                                                                                                                                                                                                                                               005589; Q28209;
01-FBB-1994 (Rel. 28, Created)
01-FBE-1994 (Rel. 28, Last sequence update)
01-FBE-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and tPA.";

Int. Dairy J. 5:605-617(1995).

-! CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

-! INDUCTION: By retinoic acid.

-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-! SIMILARITY: Contains 1 kringle domain.

-! SIMILARITY: Contains 1 BGP-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Bovine urokinase-type plasminogen activator and its receptor: cloning and induction by retinoic acid.";
Gene 125:177-183(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Aortic endothelium;
MEDLINE=93216119; PubMed=8385052;
Kraetzschmar J., Haendler B., Kojima S., Rifkin D.B.,
Schleuning W.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ravn P., Berglund L., Petersen T.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.231; -.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, L01546; AAA51419.1, -.
EMBL, X85801; CAA59796.1; -.
PIR; JNO560; JNO560.
HSSP; P00749; 1LMW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Kidney;
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72 CYQGNGHSYRGKANRDLSGRPCLAWDSPTVLLKMYHAHRSDAIQLGLGKHNYCRNPDNQR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 KPWCHVLKNRRLTWEYCDVPSCST------CGLRQYSQPQFRIKGGLFADIA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 TRGEMQFEVEKLILHEDYSAESLAHHNDIALLKIRTSRGQCAQPSRSIQTICLPPEHEDA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 GEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 PDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRS 312
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INTERCHAIN (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
A -> T (IN REF. 2).
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CHAIN A (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
EGF-LIKE.
KRINGLE.
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Kringle, EGF-like domain, Signal, Zymogen.
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InterPro; IPR006209; EGF like.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00725; CHYOUTRYSIN.
PRINTS; PR007018; KRINGLE.
ProDom; PR0010395; KR; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; EGF 1; 1.
PROSITE; PS00121; EGF 1; 1.
PROSITE; PS00134; RRINGLE 2; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
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Best Local Similarity
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373 NMR 375 : | 424 HTR 426

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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**Sp rodent: *

**Sp virus: *

**Sp vertebrate: *

**Sp unclassified: *

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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SOMMAKIES	rth DB ID Description	4	4 O9BZW1	6 088023	11 Q91VP2	6 Q8MKB1	ø	6 Q8MHY7	13 Q90675	11 Q8VCS4	560 4 Q14520 homo sapien	11 Q8K0D2	4 Q81ZZ5	11 035727	6 097507	11 091WJS	
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de	~ -	95.	94	81.0	77.	74.	37	37.	•	•				•	. ,	•	
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806 6 018783 810 4 Q15146 334 6 046507 854 6 046506	. F 4 0	114	90 4 Q8NG20 802 4 Q8IUE2 811 4 Q8IU80	5 11	214 6 Q9XT70 607 13 Q91001 267 5 Q9BK47	371 11 Q8CJ16 445 11 Q8CJ17 471 11 Q8CFE0 505 5 0966V4	4412511
580 28.1 560.5 27.2 555.5 27.0	23.7 23.7 22.5	453 22.0 452 21.9 449 21.8	443.5 21.5 443.5 21.5 443.5 21.5	442.5 21.5 433.5 21.0 427.5 20.7	<b>ល់ ល់ ល់</b>	422 20.5 422 20.5 416.5 20.2 415.5 20.2	1999 1999 1999 1995
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## ALIGNMENTS

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OBBURGA

OL-JUN-2001 (TREMBLEE]. 17, Created)

DT 01-JUN-2001 (TREMBLEE]. 17, Last sequence update)

DT 01-JUN-2001 (TREMBLEE]. 17, Last sequence update)

DE SIMILAR LOOD (TREMBLEE]. 13, Last sequence update)

DE SIMILAR LOOD (TREMBLEE]. 13, Last sequence update)

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OC BURGA FOR (Human).

OC BURGA FOR (Human).

OC BURGA FOR MA.

RA STRAUBBERG R.;

RA STRAUB PROFOCO 1 MAGH.

DR HASP: POOTOO 1 MAGH.

DR PEARL; PROFOCO 1 MAGH.

DR PEARL; PROFOCO 1 MAGH.

DR PEARL; SMOOTO 1 MAGH.

DR PRANTS; SMOOTO 1 MAGH.

DR SWART; SMOOTO 1 MAGH.

DR SWART; SMOOTO 1 MAGH.

DR SWART; SMOOTO 1 MAGH.

DR PROSITE; PROFOCO 1 MAGH.

DR PROSIT

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NCBI_TaxID=9823;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Neonatal thrombolytic agent alpha-form (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease
                                                                                                                                                                                               Length 516;
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SEQUENCE FROM N.A.

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--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
--- SIMILARITY: CONTAINS I KRINGLE DOMAIN.
EMBL; PEZGG025; AAX11956.1; --
HSSP; POO750; 1PK2.
INTERPO: IPRO01031; Fibrnctni.
INTERPO: IPRO01031; Fibrnctni.
INTERPO: IPRO01031; Fibrnctni.
INTERPO: IPRO01034; Ser_protease_Try.
Feam; PFO0039; fini; 1.
Remis PF00039; Kringle; 1.
RPINTS; PR00122; CHYMOTRYPSIN.
RPINTS; PR00122; CHYMOTRYPSIN.
RPINTS; PR00129; Kringle; 1.
SWART; SW00020; FN1; 1.
SWART; SW00020; Tryp SPC; 1.
RPROSITE; PS00021; KRINGLE_1; 1.
RPROSITE; PS00021; KRINGLE_1; 1.
RPROSITE; PS00021; KRINGLE_1; 1.
                                                                                                                                                                                             95.1%; Score 1961; DB 4;
99.7%; Pred. No. 5.4e-187;
iive 0; Mismatches 1;
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Best Local Similarity 99.79
Matches 355; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                 94.2%; Score 1942; DB 4; Length 395; 99.2%; Pred. No. 3e-185; Live 0; Mismatches 3; Indels (
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
NON TER 395
SEQÜENCE 395 AA, 44323 MW; 3FBD4A2F0B7C11C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Enamel organ;
TISSUE=En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-plasminogen activator.
Suss scrofa (Pig).
Eukaryots, Merszoa, Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562
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SMART; SM0181; BGF; 1.
SMART; SM00181; FN1; 1.
SMART; SM00130; KR; 2.
SMART; SM0020; TryP, SPC; 1.
PROSITE; PS00126; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.29
Matches 351; Conservative
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Gaps

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204 ACPKGKSEDCYVGKGVTYRGTHSLTTSQASCLPWNSIVLMGKSYTAWRINSQALGLGRRHN 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 YCRNPDGDARPWCHVMKDRKLTWBYCDMSPCSTCGLRQYKRPQPRIKGGLYTDITSHPWQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 KFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 TFEIEKYIVHEEFDDDTYDNDIALLQLRSQSKQCAQESSSVGTACLPDPNLQLPDWTECE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AASEGNS-DCYFGNGSAYRGTHSLIESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 HDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMR 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue-type plasminogen activator.
Oydtolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                        domain; Glycoprofein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Sugiki M., Yoshida E., Anai K., Maruyama M.;
Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
-!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
EMBL; AY029518; AAK40240.1; -.
InterPro; IPR006209; EGF like.
InterPro; IPR006093; Pibrnctn1.
                                                                                                                                                                                                                                                                            559 AA; 63122 MW; 8CCER2BDB94514D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                          Query Match 77.7%; Score 1601; DB 11; Best Local Similarity 79.5%; Pred. No. 5.5e-151; Matches 283; Conservative 34; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $
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InterPro; IPR0010011; Kringle.
InterPro; OPR001054; Ser_protease_Try.
Pfam; PF00008; EGF, 1.
              PRODOM; PD000395; Kringle; 2.
SWART; SW00181; EGF; 1.
SWART; SW00181; EGF; 1.
SWART; SW001008; FN1; 1.
SWART; SW00100; Tryp SPC; 1.
PROSITE; PS00102; EGF 1; 1.
PROSITE; PS010186; EGF 2; 1.
PROSITE; PS01023; FIBROWSCTIN 1; 1.
PROSITE; PS00021; KRINGLE 1; 2.
PROSITE; PS00021; KRINGLE 1; 2.
PROSITE; PS00013; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
EGF-like domain; Glycoprofein; Hydrol. Serine protease.
SEQUENCE 559 AA; 63122 MW; BCCEE2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Q8MKB1
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                                                                                                                                                                                                                                                                                                                                                                                                 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                        AASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNY
                                                                                                                                                                                                                                                                       207 ACTKEKEECYTGKGLDYRGTRSLTMSGAFCLPWNSLVLMGKIYTAWNSNAQTLGLGKHNY
                                                                                                                                                                                                                                                                                                         CRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEVEKYIVHKEPDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP 376
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                        ö
 PROSITE; PS50070; KRINGLE 1; 2.
PROSITE; PS50070; KRINGLE 2; 2.
PROSITE; PS5014; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; SEQUENCE 562 AA: 67660 ...
                                                                                                                                                                        Length 562;
                                                                                                                                                                   ttch 81.0%; Score 1669; DB 6; Length 5 sal Similarity 82.0%; Pred. No. 8.9e-158; 292; Conservative 27; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similar to plasminogen activator, tissue. PLAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR000001; Kringle.
PR001254; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
FIBRONECTIN 1; 1
KRINGLE 1: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:97610; Plat.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000529; BGF_like.
InterPro; IPR000683; Fibrnctnl.
InterPro; IPR006510; IBGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 1.
Pfam; PF00039; fn1; 1.
Pfam; PF00051; kringle; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Breast tumor;
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01-DEC-2001 (
01-MAR-2003 (
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PROSITE,
PROSITE,
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PROSITE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                     Query Match
Best Local
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RESULT Q91VP2

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250 TPG--EMKFEVEQLILHEGYSADTLAHHNDIALLKILSNNGQCAQPSRSIQTICLPPWNA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRT--YRV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 VPGEBEOKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPPADL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 QLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 RSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYHGDGHSYRGKANTDIMDRPCLAWNSANVLTKTYHAHRPDALQLGLGKHNYCRNPDHQR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPNFGTSCEITGFGKENSTDYLYPEQLKMTVVKLVSYQECQQPHYYGSEVTTKMLCAAD-
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.3%; Score 769; DB 6; Length 43 Best Local Similarity 43.1%; Pred. No. 4.9e-68; Matches 157; Conservative 52; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00021; KRINGLE 2; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN ER; 1.
PROSITE; PS00135; TRYPSIN ER; 1.
SRQUENCE 4:33 AA; 48375 MW; 65E64F36415549B0 CRC64;
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Last annotation update)
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UROKINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00022; EGF_1; 1.
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RSHI 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 AEEEQIFEVEQPILHERFDEGTYDNDIALLKLKSTSGSCAQESQAVRLVCLPDASLQLPD 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AQVNLHDACQCDSGGPLVCMTDGHWTLIGIISWGLGCGQKDVPGVYTKVVNYLGWIQQHV 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGG 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 FATVAQAASEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALG
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NCBL_TaxID=9986;
                           | Promise | Process | Proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.5%; Score 1536; DB 6; Length 564; 75.7%; Pred. No. 1.7e-144; ive 29; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22155945; PubMed=12149463;
Falkenberg M., Tom C., DeYoung M.B., Wen S., Linnemann
Dichek D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564 AA; 62726 MW; 459D8BAC6D4A937C CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PLAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 75.78
Matches 274; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease.
SEQUENCE 564 A
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             Pfam; PF00039;
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Gaps

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Serine protease.

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01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Tissue-type plasminogen activator (Fragment).
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Matches 130; Conservative
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                                                                                                                                             Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=White Leghorn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
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TISSUE=Liver;
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SEQUENCE
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Q8VCS4;
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     SOT THE PRESENCE OF THE PRESEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 SHPWQAALFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRT--YRV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 VPGEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPPADL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 RSGGPQANIHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 ----PQWET-DSCQGDSGGPLVCSVQGRMTLTGIVSWGRGCALKNKPGVYTRVSRFLPW1 421
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SMART; SM00120; Tryp_SPc; 1.
PROSITE; PS00021; EGF 1; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00031; KRINGLE 2; 1.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS500134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_BRS; 1.
Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SEQUENCE 433 AA; 48444 MW; 6DD35A371010A6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
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43.1%; Pred. No. 7.8e-68;
ive 52; Mismatches 127; Indels
                          SEQUENCE FROM N.A.
Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q90675
Q90675;
01-NOV-1996 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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83 NPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 NPDGDAQPWCHVWKDRQLTWEYCDVPQCVTCGLRQYKRPQFRIKGGLFADITSHPWQAAI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 AEEDGDCYTGNGLAYRGTRSRTKSGFSCLPWNPVFLTSKIYTALEEQRRALGLGKHNHCR 94
                                                                                                                                                                                                              MEDLINE=97199025; PubMed=9047000; Johnson A.L., Bridgham J.T., Anthony R.V.; Johnson A.L., Bridgham J.T., Anthony R.V.; Expression of avian urokinase and tissue-type plasminogen activator messenger ribonucleic acid during follicle development and atresia."; Biol. Reprod. 56:581-588(1997).
-- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
-- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
HSSP; PO0750; IRTF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 SEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCR
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.0%; Score 763; DB 13; Length 202; 77.4%; Pred. No. 7.1e-68; tive 16; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Hydrolase; Kringle; Protease; Serine protease. NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 202
202 AA; 23148 MW; 049DB42941DB3AFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               MERODS; SOL.232; --.
InterPro; IPRO00001; Kringle.
InterPro; IPRO10254; Ser_protease_Try.
Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0018; KRINGLE.
PRODOM; PRO00395; Kringle; 2.
SWART; SM00130; KR; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50040; KRINGLE 2; 2.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DIM; 1.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 OPOFRIKGGLFADIASHPWOAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 HHLTVILGRTYRVVPGEEEQKFEVEKYI---VHKEFDDDTYDNDIALLQLKSDSSRCAQE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFVOPICLPEAGSSFPTGHKCQIAGMGHMDENVSSYSNSLLEALVPLVADHKCSSPEVY 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 NRTVTDNMLCAG--DTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO1253; FIBRONECTIN 1; 1.
PROSITE; PSO1253; FIBRONECTIN 1; 1.
PROSITE; PSO1023; FIBRONECTIN 2; 1.
PROSITE; PSO1021; KRINGLE 1; 1.
PROSITE; PSO1034; TRYPSIN DOW; 1.
PROSITE; PSO134; TRYPSIN DOW; 1.
PROSITE; PSO135; TRYPSIN SER; 1.
HYPOTHETICAL PROTECTIN; EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SEQUENCE 653 AA; 70553 MW; FE18D90174ED6FDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.0%; Score 742.5; DB 11; Length 653; Best Local Similarity 40.1%; Pred. No. 3.8e-65; Matches 153; Conservative 58; Mismatches 118; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 KPWCHVLKNRRLTWEYCDVPSCS-----
                                                                                                                                               Kringle.
Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVPGVYTKVTNYLDWIRDNMRP 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |||||:| ||:||| :||
NKPGVYTRVANYVDWINDRIRP 645
                                                      InterPro; IFROO'12; ESF_like.
InterPro; IFROOO83; Fibrnctnl.
InterPro; IFROOO83; Fibrnctnl.
InterPro; IFROOO83; Fibrnctnl.
InterPro; IFROOO810; Kringle.
InterPro; IFROOO815; Ser_protease.
Ffam; PFOOO09; EGF; 2.
Ffam; PFOOO09; Fnf; 1.
FRINTS; PROOO13; KAINGLE.
FRINTS; PROOO13; KAINGLE.
FRINTS; PROOO19; KRINGLE.
FRODOM; PDOOO395; FN TYPE II; 1.
                      Chymotrypsin.
                                           EGF 2.
EGF like.
Fibrnctnl.
                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00181; EGF; 2.
SMART; SM00130; FN2; 1.
SMART; SM00130; KR; 1.
SMART; SM0020; Tryp SPC; 1.
PROSITE; PS01186; EGF_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
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SOW WAY WAS A STANFORD TO BE A STANFORD 
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560 AA.

PRT;

PRELIMINARY;

Q14520 PREI Q14520; O00663;

RESULT 10 Q14520 ID Q1452 f.C Q1452

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10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 QF-RIKGGLFADIASHPWQAAIFAK--HRRSPGERFLCGGILISSCWILSAAHCFQERFP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : || || : || || 310 KIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTAAHCTD--IK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TCGLRQYSQP 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Purification and characterization of a novel hyaluronan-binding
protein (PHBP) from human plasma: it has three EGF, a kringle and
serine protease domain, similar to hepatocyte growth factor
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
102. Homo sapinas (Hyaluronan binding protein 2).
103. Homo sapinas (Hyaluronan binding protein 2).
103. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
103. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
103. MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
MEDLINE=96425001; PubMed=8827452;
Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prodom; P0000395; Kringle; 1.
PROSITE; P8000295; Kringle; 1.
PROSITE; P8000201; KRINGLE 1; 1.
PROSITE; P800021; KRINGLE 2; 2.
PROSITE; P850040; KRINGLE 2; 1.
PROSITE; P850040; TRYPEIN DOM; 1.
PROSITE; P800134; TRYPEIN HIS; 1.
PROSITE; P800135; TRYPEIN ERE; 1.
PROSITE; P800135; TRYPEIN ERE; 1.
PROSITE; P800135; TRYPEIN SER; 1.
SGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SEQUENCE 560 AA; 62671 MW; 5C1907230784ACD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kitamura N.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGDAKPWCHV-LKNRRLTWEYCDVPSCS-------
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34.4%; Score 709.5; DB 4;
Best Local Similarity 39.1%; Pred. No. 6.1e-62;
Matches 148; Conservative 62; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WERRY, SOI. 033; -...
Genew; HGNC: 4798; HABP2.
Genew; HGNC: 4798; HABP2.
InterPro; IPR006209; EGF like.
InterPro; IPR000001; Kringle.
InterPro; IPR00008; Ker_Drotease_Try.
Pfam; PF00008; EGF; 3.
Pfam; PF00008; Kringle; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. 119:1157-1165(1996)
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PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Colon, and Kidney;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SRYVKTVCL-PSD-PFPSGTECHISGWGVTETGEG--SRQLLDAKVKLIANPLCNSRQLY 440
                                                                                                                                                   236
                                                                                                                                                                                               384
                                                                                                                                                                                                                                           SSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPPYSERLKEAHVRLYPSSRCTSQHLL 296
                                                                                                                                                                                                                                                                                                                                                                 NRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 WGHS-----FCAGSLIAPCWVLTAAHCLQDRPAPEDLTVVLGGERRNHSCEPCQTLAV 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445 RSYRLHEAFSPVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVAG 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 QF-RIKGGLFADIASHPWQAAIFAK--HRRSPGERFLCGGILISSCWILSAAHCFQERFP 178
                                                                              || || : |||| : |||| 267 AVKRIYGGFKSTAGKHPWQVSLQTSLPLTTSMPQGHFCGGALIHPCWVLTAAHCTD--IN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 EKYIVHKEFDDDTYDNDIALLQLKSDS-SRCAQESSVVRTVCLPPADLQLPDWTECELSG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 YGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDA 322
         207 DGDHKPWCFVKVNSEKVKWEYCDVTVCPVPDTPNPVESLLEPVMELPGFESCGKTEVAEH 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                179 PHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFD--DDTYDNDIALLQLKSDSSRCAQE
                                                                                                                                                                           SDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CG--LRQYSQPQFRIKGGLFADIASHPWQAAIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 AKHRRSPGERFLCGGILISSCWILSAAHCPOERPPHHLTVILGRTYRVVPGEEEQKFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83; . Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COGDSGGPLVCLN---DGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]—SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Mada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T
"Molecular chracterization of coaggulation factor XII-Mie.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB095845; BAC23095.1; -
SEQUENCE 615 AA, 67735 MW; 030508870A0C7EDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Coagnlation factor XII-Mie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.4%; Score 667.5; DB 4; 36.2%; Pred. No. 1.1e-57; tive 48; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        615
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PGVYTKVTNYLDWIRDNM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||:|| :|:||: |
PGVYTQVTKFLNWIKTTM 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 150; Conserv
                                                                                                                                                                                                                                           237
                                                                                                                                                                                                                                                                                          385
                                                                                                                                                                                                                                                                                                                                         297
                                                                                                                                                                                                                                                                                                                                                                                       441
                                                                                                                                                                                                                                                                                                                                                                                                                                   357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q81ZZ5
Q81ZZ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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TRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALE 427
                                                                       SSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLL 296
                                                                                                    NRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQXDV 356
                                                                                                                                                                                                                     536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---STCGLRQYSQP 121
                                                                                                                                                                                               25 GNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R SMART; SM00181; EGF; 3.

R SMART; SM00130; KR; 1.

SMART; SM00130; KR; 1.

SMART; SM00130; KR; 1.

R PROSITE; PS00020; Tryp_SPC; 1.

R PROSITE; PS00021; KRINGLE_1; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN SRR; 1.

R PROSITE; PS00135, TRYPSIN SRR; 1.

R PROSITE; PS00135, TRYPSIN SRR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.9%; Score 698.5; DB 11; Length 39.7%; Pred. No. 6.9e-61; ive 54; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. -! SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
11-ORT-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314; Chymotrypsin.
InterPro; IRR000184; EGF 2.
InterPro; IPR000509; EGF [2a.
InterPro; IPR006509; EGF [1ke.
InterPro; IPR006010; IEGF.
InterPro; IPR00101; Kringle.
InterPro; IPR0010154; Ser_protease_Try.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; Lrypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||:|| :|:||:
PGVYTQVTKFLNWIKATIK 555
                                                                                                                                                                                                                                                               PGVYTKVTNYLDWIRDNMR 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PP00089; trypsin; 1.
PRINTS; PR00722, CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC031775; AAH31775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissum=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150;
                           368
                                                                                                                        428
                                                                                                                                                                    297
                                                                                                                                                                                                                                                                                                              537
                                                                         237
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                                                                                                                                                                                                                                                               357
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 11

OBKODZ

10 08K0DZ

AC 08K0DD

AC 08K0DD

DT 01-0C

DT 01-0C

DT 01-MB

OC MAMM

OC MAMM

OC MAMM

OC TISS

RA SEQI

RA SEGI

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Matches
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PD000995; FN Type II; 1
PD000395; Kringle; 1.
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IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000083; Fibrncthl.
Interpro; IPR000562; FN Type_II
Interpro; IPR00010; IEGF.
Interpro; IPR000101; Kringle.
Interpro; IPR001254; Ser_protea
Pfam; PF00008; EGF; 2.
Pfam; PF00008; FGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF 2.
EGF_like.
Fibrnctnl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PR00722, CHYMOTRYPSIN
PRINTS, PR00013; FNTYPEII.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00181; BGF; 2.
SMART; SM00181; BGF; 1.
SMART; SM00189; FN1; 1.
SMART; SM00130; KR; 1.
SMART; SM00120; Tryp, SPC; 1.
PROSITE; PS00022; BGF 1; 2.
PROSITE; PS01186; BGF 2; 1.
PROSITE; PS01186; BGF 2; 1.
PROSITE; PS01186; BGF 2; 1.
PROSITE; PS01253; FIBRONECTIP
PROSITE; PS00021; KRINGLE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00040; E
                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig)
             113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVY-TAQNPSAQALGLGKHNYCRNPDGD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
559 CQGDSGGPLVCEDQAAERRLTLQGIISWGSGCGDRNKPGVYTDVAYYLAWIREH 612
                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
30.8%; Score 634.5; DB 11; Length 597;
Best Local Similarity 36.4%; Pred. No. 2.1e-54;
Matches 144; Conservative 48; Mismatches 137; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
EGF-like domain; Glycoprofein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                         Schloesser M., Schwager S., Engel W.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
--- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; X99571; CA677891.1; --
HSSP; P00760; 1AQ7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F3AC07C37D0C0FBA CRC64;
                                                                              01-0AN-1998 (TrEMBLrel. 05, Created)
01-0AN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                            597 AA
                                                                                                                                                                                                                                                                                                                  InterPro; IRR001314; Chymotrypsin.
InterPro; IRR001314; Chymotrypsin.
InterPro; IRR000639; EGF like.
InterPro; IRR000683; Fibrnctn1.
InterPro; IRR000682; FW Type_II.
InterPro; IRR000001; Kringle.
InterPro; IRR001254; Ser_protease_Try.
Pfam; PP00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01253, FIBRONECTIN 1; 1. PS00023; FIBRONECTIN 2; 1.
                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00051; kringle; 1.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMCTRYPSIN.
PRINTS; PR00013; FNTYPEII.
PRODOM; PD000995; FN TYPEII.
PRODOM; PD000995; FN TYPEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 AA; 65638 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00023; FIBRONECTIN
PS00021; KRINGLE 1; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400020; Tryp SPc; 1.
PS00022; EGF 1; 2.
PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50070; KRINGLE
                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00058; FN1; 1.
SM00059; FN2; 1.
SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00181; EGF; 2.
SMART; SM00058; FN1; 1.
SMART; SM00059; FN2; 1.
                                                                                                                                                                                                                                                                                                           MGD; MGI:1891012; F12.
                                                                                                                                                                                                                                                                                                                                                                                                                  PF00039; fn1;
PF00040; fn2;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               MEROPS; S01,211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease.
                                                                                                                   Factor XII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                          035727
                                                                     035727
                                                                                                                                                                                                                                                                                                                                                                                                                  fam;
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                                  RESULT 13
035727
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-----CG--LRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILIS 162
                                                   333 LSKTNTMGCGORFRKGLSSFMRVVGGLVALPGSHPYIAALYW-----GNNF-CAGSLIA 385
                                                                                                                163 SCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIA 222
                                                                                                                                                                                                                                   223 ILQL-KSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 281
                                                                                                                                                                                                                                                                                                                                                282 VRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVC---LNDGR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

TISSUB-Liver;

Takahashi T., Kihara T.;

"Porcine liver factor XII.";

Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: COTTAINS 1 KRINGLE DOMAIN.

EMBL; AB022425; BAA37148.1; -.

HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 MTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ser_protease_Try.
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InterPro; IPR000742; EGF_2.
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completed: August
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Job time : 41 secs
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                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                      331 TPSQNLTSAWCAPPEQRGPLPSAGLVGCGQRLRKRLSSLNRIVGGLVALPGAHPYIAALY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKYIVHKEPDDDTYDNDIALLQLKSDSSR-CAQESSVVRTVCLP--PADLQLPDWTECEL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CG--LRQYSQPQFRIKGGLFADIASHPWQAAIF 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLH 320
                                                                                                                                                                                                                                                                                                                                                                                      CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSA-QAL--GLGKHNYCRNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 AGWGHQFEGAEEYSSFLQEAQVPLISPERCSAADVHGAAFTPGMLCAGFLEGG----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DACQGDSGGPLVCLN---DGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/Sv;
Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
                                                                                                                                                                                                                                  90;
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN EBR; 1.
EGF-like domain; Glycoprofein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagaraja R.; "Genomic Sequence Analysis in the Mouse t-complex Region."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              48; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                       616 AA; 68012 MW; 4C5FE3D71EBBD1A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                              GDAKPWCHVLKNRRLTWEYCDVPSCST------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                 30.6%; Score 630; DB 6 35.8%; Pred. No. 6e-54;
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MSD; MGI-97620; P19.
InterPro; IPR001314; Chymotrypain.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC014773; AAH14773.1; -. EMBL; AF481053; AAM22156.1; -.
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(TrEMBLrel. 19, I
(TrEMBLrel. 23, I
                                                                                                                                                                                                                              Matches 149; Conservative
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                                                                                                                                                                                                         Local Similarity
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                                                                                                             Serine protease
SEQUENCE 616
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01-DEC-2001 (
01-MAR-2003 (
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PLG.
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1D 091WJ1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 FPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQE 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738 NNRVKSTELCAGOLAGG-----VDSCOGDSGGPLVCPEKDKYILOGVTSWGLGCARPNK 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 TVSQEPSGPSDSETDCMYGNGKDYRGKTAVTAAGTPCQGW-----AAQEPHRHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 FIPQINPRAGLEK-NYCRNPDGDVNGPMCYTTNPRKL-YDYCDIPLCASASSFEGGKPQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                             Prodom; P0000395; Kringle; ·5.
PROSITE; PS00021; KRINGLE 1; 5.
PROSITE; PS000318; SCMATNGLE 2; 5.
PROSITE; PS000318; SCMATNGLE 2; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN ESE; 1.
Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.5%; Score 607; DB 11; Length 8 36.7%; Pred. No. 1.7e-51; ive 54; Mismatches 132; Indels
InterPro; IPR001966; Prothrombin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001400; Somatotropin.
                                                                         Pfam; PF00051; kringle; S. Pfam; PF00024; PAN; 1. Pfam; PF00089; trypsin; 1. PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR01505; PROTHROMBIN.
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PGVYVRVSRFYDWIEREMR
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Matches 139; Conservative
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Searched:	2888711 segs, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422

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31: em\_htg\_other:\*
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38: em\_htg\_pln:\*
39: em\_htg\_other:\*
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40: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	AKIES	Description	AX430829 Sequenc	AX431269 Sequenc	X4312/2 Sequence X95748 Synthetic	X95747 Synthetic	X95749	31 X95750 Synthetic	AX431268	AA4312/1 AP268280	AR241678 Sequence	AP26828	AX591634	AX600065	AX554424 AX554413	AX554422	AX642149	AX55442	L42764 (		E02814	E03955 DNA	AX236721 Sequenc 108200 Semience			AR179433 Sequence			AX034619 Sequence					AX191724	000307 E. COLI OMD A08458 pinf 4-49 m	AJ223121 Artifici	2 AJ223122	AE000198 E	AE005286 F	alignments		bo DNA linear DAT 28-,TIN-2002	6.			a coli Proteobacteria; Gammaproteobacteria; Enterobacteriales; eriaceae; Escherichia.	Tavaniwatana C Manosroi A. and Manosroi J	uction in prokaryotes
	SUMMARIE	OI .	AX430829	AX431269		HSIGKLO	HSIGKLC14		AX431268	AX4312/1	AR241678	AF26828	AX591634	AX600065	AX554424	AX554422	AX642149	AX554420	STAFRA	AX 74 2885 AX 74 3 5 0 9	E02814	E03955	AX236721	152035		AR179433	AK282580	AX030798	AX034619	E01685	AF234271	STOMPA	AF234269	AX191724	ACCAPA AOS458	ASAK31	ASAK31	AE000198	200	ALIGN		99	Patent W0024069	806		eria; Gam Escherich	Tavani	, je,
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	غ مه	Score Ma	66 100	66 100		66 100							66 100.0		99			99	4.	7.7	2.0	2.5	2.0		0.2	2.5	9.0	. 6	60.2 91	2.0	7 0	. 0	0.5	2.5	7.0	. 7	0.2	9.50	7.			AX430829	Sequen	AX430829 AX430829.	Escherichia	Bacteri Enterob	Goetz	Methods
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105 bp mRNA linear SYN 29-MAR-2001
Synchetic construct including Homo sapiens immunoglobulin kappa
chain (clone: 28).
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Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General &
Experimental Pathology, General Hospital, Wachringer Guertel 18-20,
 Methods for large scale production of recombinant dna-derived tpa
or k2s molecules
Patent: WO 0240650-A 6 23-MAY-2002;
BOEHRINGER INGELHEIM INT (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                 Steinberger, P., Kraft, D. and Valenta, R.

Construction of a combinatorial IgE library from an allergic
patient. Isolation and characterization of human IgE Pabs with
specificity for the major timothy grass pollen allergen, Phl p
J. Biol. Chem. 271 (18), 10967-10972 (1996)
                                                                                                                                                                                                                               Gaps
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constant region; immunoglobulin; kappa light chain.
synthetic construct
synthetic construct
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                                                                                                                                                                                               Length
                                                                                                                                                                                              Score 66; DB 6; I
Pred. No. 1.4e-11;
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/organism="synthetic construct"
/moi_type="mRNA"
/db_xref="taxon:32630"
                                                                                                    coli"

    .66
    /organism="Escherichia coli"
/mol_type="mRNA"
    /db_rref="taxon:562"

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                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:562"
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/db_xref="taxon:9606"
/clone="28"
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Location/Qualifiers
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/codon_start=1
/transl_table=11
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1. Similarity 100.0%;
66; Conservative 0;
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Valenta, R.L.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goetz, F., Werner, R.G., Tayapiwatana, C., Manosroi, A. and Manoëroi, J., Methods for large scale production of recombinant dna-derived tpa or k2s molecules
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 66; Conservative 0; Mismatches 0;
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/db_xref="taxon:562"
                                                  coli"
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BOEHRINGER INGELHEIM INT (DE)
Location/Qualifiers
                            1. .66
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Sequence 6 from Patent WO0240650.
AX431272
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Sequence 3 from Patent WO0240650
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BOEHRINGER INGELHEIM INT (DE)
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AX431272
                FEATURES
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Valenta, R.L.S.
Direct Submission
Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General &
Experimental Pathology, General Hospital, Waehringer Guertel 18-20,
1090 Vienna, AUSTRIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="WKKTAIAIAVALAGFATVAQAAELTQSPSSVSASVGDRVTITCR
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PREAKVQMKVDNALQSGNSQESVTFGDDSKDSTYSLSSTLTLSKADYEKHKLYACEVTH
QGLSSPVTKSFNRGEC"
Steinberger, P., Kraft, D. and Valenta, R.
Construction of a combinatorial IgE library from an allergic
patient. Isolation and characterization of human IgE Fabs with
specificity for the major timothy grass pollen allergen, Phl p i
J. Biol. Chem. 271 (18), 10967-10972 (1996)
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/gene="OMP-A"
/note="SAC 1 restriction site"
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'note="PCR-primer sequence"
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1. .705
'gene="OMP-A"
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/clone_lib="pcomb3H'
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/gene="OMP-A"
/note="FR1"
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163. .207
/qene="OMP-A"
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/note="CDR3"
352. .384
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                                                                                           /translation="wkktyalalgraturggareltgebesleagygdrutter asgsilgylungtongreteriality assignmental translation assignment as
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     product="immunoglobulin kappa light chain"

'protein id="CAA65059."

'db_xref="GI:1514579"

'db_xref="REMTREMBL:CAA65059"
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constant region; immunoglobulin; kappa light chain.
synthetic construct
synthetic construct
artificial sequences.
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100.0%; Pred. No. 1.6e-11;
tive 0; Mismatches 0;
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note="SAC 1 restriction site"
30. 1162
gene="OMP-A"
note="CDR1"
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| gene="OMP-A"
| note="kappa constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PCR-primer sequence"
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/gene="OMP-A"
/note="FR1"
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208. .228
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/gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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Best Local Similarity 100.
Matches 66; Conservative
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/tränslation="MKKTAIAIAVALAGFATVAQAAELVWTGSPSSLSASVGDRVTIT
CASHSISINSYLMYQQKPRAPKLLITAAASSLGSGVBRRFSGSGSGTPTLTISSLQP
EDRANYCQESFSPSGGTFGGGTKVBIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLIN
FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKLYACEV
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Systype 1 (2000: 31).
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Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                 note="SAC 1 restriction site"
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/gene="OMP-A"
/note="FR1"
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gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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note="CDR1"
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Valenta, R.L.S.
Direct Submission
Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General & Experimental Pathology, General Hospital, Wachringer Guertel 18-20, 1090 Vienna, AUSTRIA
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Construction of a combinatorial IgE library from an allergic
patient. Isolation and characterization of human IgE Fabs with
specificity for the major timothy grass pollen allergen, Phl p
J. Biol. Chem. 271 (18), 10967-10972 (1996)
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/transl_table=11
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/gene="Gure ...
/note="FR4"
385. .702
/gene="CMP-A"
/note="Kappa constant region"
661. .705
/gene="CMP-A"
/note="PCR-primer sequence"
/note="PCR-primer sequence"
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    .66
    /organism="Escherichia coli"
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    /db_xref="taxon:562"

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/clone_lib="pcomb3H"
1. .711
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PAT 28-JUN-2002
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Methods for large scale production of recombinant dna-derived tpa
or k2s molecules
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/db_xref="taxon:32630"
/note=="coding sequence for OmpA-KZS fusion protein"
332 c 332 g 226 t
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              391..708
/gene="OMP-A"
/note="Aappa constant region"
667..708
/gene="OMP-A"
/note="PCR-primer sequence"
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BOEHRINGER INGELHEIM INT (DE)
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      'note="FR4"
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FYPREAKVQMKVDDALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
THQGLSSPVTKSFNRGEC"
                                                                                          2 (bases 1 to 711)
Valenta,R.L.S.
Direct Submission
Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General &
Experimental Pathology, General Hospital, Waehringer Guertel 18-20,
1090 Vienna, AUGTRIA
Construction of a combinatorial IgE library from an allergic patient. Isolation and characterization of human IgE Fabs with specificity for the major timothy grass pollen allergen, Phl p J. Biol. Chem. 271 (18), 10967-10972 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/db_xref="GI:1514583"
/db_xref="GI:1514583"
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/gene="OMP-A"
/note="SAC 1 restriction site"

    .66
    /organism="Escherichia coli"
|mol_type="mRNA"
    /db xref="taxon:562"

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                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="B-cell"
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1. .711
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                                                                                                                                                                                                                                                                                                                                                                            'mol_type="mRNA"
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358. .390
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/gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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gene="OMP-A"
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Direct Submission
Submitted (16-MAY-2000) Department of Molecular Biology, BCC-526,
Scripps Research Institute, 10550 N. Torrey Pines Rd., La Jolla, CA
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                                                                                              1 (bases 1 to 3450)
Janda, K.D., Wirsching, P., Lerner, R.A. and Gao, C.
Wethods for display of heterodimeric proteins on filamentous phage
using pVII and pIX, compositions, vectors and combinatorial
libraries
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Phagemid cloning vector pComb3X
artificial sequences; vectors.

1 (bases 1 to 3758)
Rader, C. and Barbas, C.F. III.
(in) PHAGE DISPLAY, A LABORATORY MANUAL. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, USA (2000), In press Rader, C. and Barbas, C.F. III.
Rader, C. and Barbas, C.F. III.
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1. 3758
/organism="Phagemid cloning vector pComb3x"
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1 896 c 959 g 964 t
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Phagemid cloning vector pComb3X, complete sequence.
AF268281
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100.0%; Pred. No. 1.7e-11;
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Location/Qualifiers
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799 c 891 g
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Matches 66; Conservative
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Matches 66; Conservative
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artificial sequences; vectors.

1 (bases 1 to 3)34)
Rader,C. and Barbas,C.F. III.
(in) PHAGE DISPLAY, A LABORATORY MANUAL. Cold Spring Harbor
Laboratory Press, Cold Spring Harbor, NY, USA (2000), In press
2 (bases 1 to 3)34)
Rader,C. and Barbas,C.F. III.
Direct Submission
Submitted (16-MAY-2000) Department of Molecular Biology, BCC-526,
Scripps Research Institute, 10550 N. Torrey Pines Rd., La Jolla, CA
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Patent: WO 0240650-A 5 23-MAY-2002;
BOEHRINGER INGELHEIM INT (DE)
Location/Qualifiers
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/db xref="taxon:32630"
/db zecef-"taxon:33630"

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-783 C 876 G 873 t
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Sequence 20 from patent US 6472147.
AR241678.1 GI:27287480
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Matches 66; Conservative
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TITLE JOURNAL

FEATURES

REFERENCE AUTHORS BASE COUNT

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 10 AF268280

PAT 27-JAN-2003

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PAT 27-NOV-2002

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Bowdish, K.S., Barbas-Frederickson, S., Wild, M. and Mcwhirter, J. Novel plasmid vectors
Novel plasmid vectors
Patent: NO 0246436-A 12 13-JUN-2002;
ALEXION PHARMACETITALS, INC. (US)
Location/Qualifiers
Sequence 12 from Patent W00246436.
AX554424
                                                AX554424.1 GI:25898200
                                                                                              synthetic construct artificial sequences.
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Patent: WO 0246238-A 60 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 66; Conservative 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                  Novel plasmid vectors
Patent: WO 0246434-A 8 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 60 from Patent W00246238.
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   Sequence 8 from Patent WO0246434.
AXS91634
                             AX591634.1 GI:27950030
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Plasmid pRL8 nucle
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and is derived by analysis of the total score distribution.
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Omp A signal pepti
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Kappa light chain
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GM212 single chain
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DNA encoding TLHL.
Plasmid pBBP20 DNA
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Bilin binding-prot
Bilin binding-prot
Plasmid pBBP20 DNA
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Plasmid pBBP21 DNA
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XS; cardidac infearction; acute mycoardial infarction; pulmonary embolism; 
artery occlusion; deep vein thrombosis; blood clotting; thrombolytic; 
cerebroprotective; cardiant; ompA; gene; ds.
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/*tag= a
/product= "OmpA peptide"
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RESULT 3
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                                                                                                                                                                                                                                                                                                 The present invention relates to a method of producing extracellularly secreted, active, correctly folded, recombinant tissue plasminogen activator (tPA). Kringle 2 serine protease molecule (KS2) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vain thrombosis or related diseases associated with unwanted blood clotting. The present sequence is a supplying the occlusion of the present sequence is a supplying the occlusion of the present sequence is a supplying the prese
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                                                                                                                                                              Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
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                                                             Manosroi A;
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                                                           Tayapiwatana C, Manosroi J,
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2.1e-14;
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Matches 66; Conservative
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P-PSDB; AAE25035.
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                                                           Werner R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD38987;
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AAD38987
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The invention relates to a method for producing recombinant DNA-derived heterologous protein in prokaryotic cells, where the heterologous protein is secreted extracellularly as an active and correctly folded protein and
                                                                                                                                                                                                                             the prokaryotic cell contains and expresses a vector comprising the DNA coding for the heterologous protein operably linked to the DNA coding for the signal peptide OmpA or its functional derivative. The method is useful for commercial large-scale production of heterologous proteins, e.g. K2S (kringle 2 plus serine protease), in prokaryotic cells, and is generally applicable in the expression of several different proteins and polypeptides which do not require mammalian glycosylation in prokaryotic host cells. The method may also be used to obtain DNA sequences of a protein of interest to be expressed from databases and cloned for use.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTTCGCTACCGTGGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing recombinant DNA-derived kringle 2 plus serine protease, comprises using a prokaryotic cell expressing a vector having a DNA coding for a heterologous protein operably linked to a DNA coding for the signal peptide OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue plasminogen activator; tPA; kringle 2 serine protease; stroke; K2S; cardiac infarction; acute myocardial infarction; pulmonary embolartery occlusion; deep vein thrombosis; blood clotting; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manosroi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "OmpA-K2S fusion protein"
/transl except= (pos:1126..1128, aa:Pro-Gly)
/note= "No stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 66; DB 24; Length 66; 100.0%; Pred. No. 2.1e-14; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cerebroprotective; cardiant; ompA; fusion protein; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goetz F, Tayapiwatana C, Manosroi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is Escherichia coli OmpA DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66 BP; 14 A; 18 C; 21 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OmpA-K2S fusion protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                  Claim 9; Page 23; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD40614 standard; DNA; 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-2000; 2000GB-0027779.
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2002.
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                                                                                                              The present invention relates to a method of producing extracellularly secreted, active, correctly folded, recombinant tissue plasminogen activator (tPA), Kringle 2 serine protease molecule (Kr2) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants. Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded attention across across and account of the proposition of the proposition are proposed attentions.
                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                       Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
                                                                                                                                                                                                                                              diseases associated with unwanted blood clotting. The present sequence is a DNA encoding a fusion protein comprising OmpA and K2S protein.
                                                                                                                                                                                                                                                                                                                                                        Erythrocyte; Hepatitis B; dual-specific antibody; surface antigen; ds.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a dual-specific antibody composed of the surface antigens to resist against erythrocyte and hepatitis B,
                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythrocyte and Hepatitis B dual-specific antibody DNA sequence
                                                                                                                                                                                                                                                                                                           100.0%; Score 66; DB 24; Length 1128; 100.0%; Pred. No. 4.3e-14; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic engineering double specific antibody and its use
                                                                                                                                                                                                                                                                                   Sequence 1128 BP; 238 A; 332 C; 332 G; 226 T; 0 other;
                                                                                           Claim 7; Page 30; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ57599 standard; DNA; 1574 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 1-2; 6pp; Chinese
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                                                                                                                                                                                                                                                                                                                                  66; Conservative
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Matches 66; Conserv
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           P-PSDB; AAE25034
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                                                                      peptide OmpA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            851
which can be used as the test reagent to detect the surface antigen recombination technique in gene engineering. The recombination technique in gene engineering. The recombination technique includes reforming the surface antigen to resist against erythrocyte and hepatitis B to become hybrid antibody genes by shortening the joining peptide of single-chain antibody, and assembling them in the same expression vector. The gene product can be directly extracted from the supernatant of bacterial culture liquid. Its advantages are low
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                    100.0%; Score 66, DB 21; Length 1574; 100.0%; Pred. No. 4.6e-14; tive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                      Sequence 1574 BP; 395 A; 390 C; 419 G; 370 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Filamentous phage; protein display; pVII; pIX; combinatorial antibody library; ds.
                                                                                                                                                                                                                                 cost, quick detection and simple operation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Janda KD, Wirsching P, Lerner RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC66993 standard; DNA; 3450 BP
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 66; Conservative
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Best Local Similarity
Local 66; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-032030/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGGCC 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector pCGMT-1b
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construct of the MT4 Fab display phagemid expression vector, pMT4-3 (see also AAQ92540), used in the invention for the production of synthetic human Fab antibodies against gpl20 of HIV.

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Seguence 4691 BP; 1170 A; 1171 C; 1232 G; 1118 T; 0 other;

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Gaps

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Indels

100.0%; Score 66; DB 16; 100.0%; Pred. No. 6.1e-14; ive 0; Mismatches 0;

Length 4691;

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This sequence represents the pComb3 phagemid expression vector. This vector has been designed to allow for anchoring of expressed proteins on the bacteriophage coat protein 3. Gene III of filamentous phage encodes the dof residue minor phage coat protein, cplII (cp3), which is expressed prior to extrusion in the phage assembly process on a bacterial membrane and accumulates on the inner membrane facing into the periphasm of E. coli. This plasmid was used within the scope of the invention to express various mutagenised human Fab's which comprise heavy and light variable regions which bind to HIV gp120. pComb3 allows for both surface display and soluble forms of the Fabs. The vector was designed for the cloning of combinatorial Fab libraries. pComb consists of a DNA molecule having two cassettes to express one fusion protein, Fd/cp3, and one soluble protein, the light chain. The finished vector comprises, commerce roperators equences, a spacer region, a cloning region bordered by 5' XhoI and 3' SpeI restriction site, a ribosome binding site (RBS), a PelB leader, a spacer region, a cloning region bordered by 5' XhoI and 3' SpeI restriction sites, the tether sequence, the sequences encoding bacteriophage cp3 followed by a stop codon, a Neal restriction site between the two cassettes, and a second lac2 promoter/operator cegion, a cloning region bordered by 5' SacI and 3' XbaI restriction sites, region, a cloning region control stop sequences and a second NotI restriction site. The pComb3 expression vector forms the basic
                                                2667 ATGAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTGGTTTCGCTACCGTGGCCCAG 2726
1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTGGTTTCGCTACCGTGGCCCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pComb3; phagemid expression vector; bacteriophage; coat protein 3; Gene III; filamentous phage; minor phage coat protein; cp11; cp3; bacterial membrane; periplasm; B. col1; human, Pab, HIV; gp120; combinatorial Pab library; cassette; Fd/cp3; lacZ promoter/operator; ribosome binding site; RBS; PelB leader; spacer; tether sequence; MT4; pMT4-3; antibody; ss; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 185-188; 249pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ92546 standard; DNA; 4691 BP.
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93US-0139409.
94US-0233619.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression vector.
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19-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoically active peptides e.g. a peptide mimetic such as an erythropoically active peptides e.g. a peptide antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to
                                                                           A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or
                                                                                                                                                                                                                                                                                                                                                                                                       TPO; BPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                        Plasmid pRL8 nucleotide sequence SEQ ID NO:60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 6A-C; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowdish KS, Barbas-Frederickson S,
                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                  ABQ73372 standard; DNA; 5149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2000; 2000US-251448P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2001; 2001US-288889P.
29-MAY-2001; 2001US-294068P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-2001; 2001WO-US47656
                                                                                                                                                                                                                                                                                                                                      (first entry)
Query Match
Best Local Similarity 100.(
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombopoetin mimetic
                                                                                                                                                                            2671 GCGGCC 2676
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                                                                                                                                             61 GCGGCC 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                    01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; ds.
                                                                                                                                                                                                                                                                                                    ABQ73372;
                                                                                                                                                                                                                                RESULT 7
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RESULT 9
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                                                                                                                                                                        2611 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTGGTTTCGCTACCGTGGCCCAG 2670
a portion of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (1) is contacted with haematopoietic stem cells or their progenitors. (1) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, disorders or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABPS1669 to ABPS1696 represent sequences used in the exemplification of the present invention.
                                                                                                                                                              9
                                                                                                                                                            1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGTTTTCGCTACCGTGGCCCAG
                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel pComb family phagemid comprising a nucleic acid encoding a dimerization domain, useful for producing antibody fragments which require dimerization in order to crosslink for activation of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "the CDS does not include a start codon"
                                                                                                                       DB 24; Length 5149;
                                                                                                 Sequence 5149 BP; 1279 A; 1244 C; 1372 G; 1254 T; 0 other;
                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                   Vector; phagemid; pRLB; pComb; dimerisation domain; Jun;
leucine zipper; antibody; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
note= "light chain stuffer region"
1968..4337
                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= b
note= "heavy chain stuffer region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Jun dimerisation domain"
                                                                                                                     100.0%; Score 66; DB 24;
100.0%; Pred. No. 6.2e-14;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barbas-Frederickson S;
                                                                                                                                                                                                                                                                      ABN84077 standard; DNA; 5149 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2001; 2001WO-US46514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-2000; 2000US-254410P
                                                                                                                                                                                                                                                                                                                                                                                                             2677..3866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4338..4583
                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product=
                                                                                                                                         66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                 Phagemid vector pRL8.
                                                                                                                                                                                                                     GCGGCC 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-537568/57.
P-PSDB; ABB79463.
                                                                                                                               Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                   99 225525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200246434-A2
                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                           ABN84077;
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                                                                                                                                                                                                                       2671
                                                                                                                      Query Match
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                                                                                                                                                                                                                                                              ABN84077
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"CH1, His6 tag, HA tag, and gene III amino acid
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                                              The present sequence is of plasmid pLR8, a pComb vector family member. pLR8 was constructed by insertion of a PCR fragment containing a flexible linker (murine kappa hinge region) followed by a Jun leucine zipper dimerisation domain into a pRL4 backbone that had been treated to remove the stuffer region. The resulting construct was then cut with restriction endomucleases to replace construct was then cut with restriction endomucleases to replace construct was then cut with restriction endomucleases to replace sector is useful in the production of biologically activity. It can also be used in the production and screening of libraries made in accordance with phage display technology. Homo-dimerisation of single chain antibodies is accomplished by the presence of the Jun leucine zipper domain, which is responsible for protein-protein interactions. Subcloning to pRU8 individually or en masse following FACS sorting or panning allows expression, e.g., of dimeric soluble Fabs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid, vector, replication, expression, foreign genetic, bacteria, cyanobacterium, Escherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT; pRL5-CAT; pRL5 bsi-CAT; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Kappa constant region amino acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 66; DB 24; Length 5149; Local Similarity 100.0%; Pred. No. 6.2e-14; nes 66; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5149 BP; 1279 A; 1244 C; 1372 G; 1254 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Beta lactamase"
Disclosure, Fig 8A-C; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pRL5 nucleic acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "pel
4740..5651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001; 2001WO-US46516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              508..3828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3859..3924
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/product=
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/product=
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591..1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2671 GCGGCC 2676
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Matches
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3110 GCGGCC 3115
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         61 GCGGCC 66
          WO200246436-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                           Bowdish KS,
                              13-JUN-2002
                                                                                                                                                                     information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL41115;
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                                                                                                                                            The invention relates to a plasmid with a nucleic acid sequence of 6122, or 5683 base pairs fully defined in the specification. The invention more specifically relates to novel vectors capable of replication and expression of foreign genetic information in bacteria, such as, for example, cyanobacterium and E. coli. The new vectors have been designed to overcome certain drawbacks of the pcombax plasmid. These new vectors include pRLS, pRLS, asc. CAT and pRLS bsi. CAT. This polymucleotide sequence represents the plasmid pRLS nucleic acid sequence
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/product= "CH1, His6 tag, HA tag, and gene III amino acid
sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid; vector; replication; expression; foreign genetic; bacteria; cyanobacterium; Escherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT;
                                                                                                                                                                                                                                                                                                        "Kappa constant region amino acid sequence"
                                                                                                                                                                                                                                                                                      Gaps
                                                                                              Novel plasmid useful in cloning and expression of foreign genetic
                                                                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                  Length 5683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "pel B leader amino acid sequence"
5179..6090
                                                Mcwhirter J;
                                                                                                                                                                                                                                              Sequence 5683 BP; 1337 A; 1495 C; 1540 G; 1311 T; 0 other;
                                                                                                                                                                                                                                                                                    Indels
                                                                            P-PSDB; AAO22536, AAO22537, AAO22538, AAO22539, AAO22542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CAT amino acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Omp A leader amino acid
                                                                                                                                                                                                                                                                 DB 24; I
6.4e-14;
hes 0;
                                                Wild M,
                                                                                                                                                                                                                                                                Query Match
100.0%; Score 66; DB
Best Local Similarity 100.0%; Pred. No. 6.4e
Matches 66; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pRLS CAT nucleic acid sequence.
                                               Barbas-frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cocation/Qualifiers
                                                                                                                            Claim 1; Fig 4A-E; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pRLS-CAT; pRL5 bsi-CAT; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                               AAL41112 standard; DNA; 6122 BP.
          08-DEC-2000; 2000US-254411P.
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                            (ALEX-) ALEXION PHARM INC
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                                                                   2002-537570/57
                                                                                                                                                                                                                                                                                                                                              99 ၁၁5525
                                                                                                                                                                                                                            the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
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                                                                                                           information
                                               Bowdish KS,
                                                                                                                                                                                                                                                                                                                                              61
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The invention relates to a plasmid with a nucleic acid sequence of 6122, 6125, or 5683 base pairs fully defined in the specification. The invention more specifically relates to novel vectors capable of replication and expression of foreign genetic information in bacteria, such as, for example, cyanobacterium and B. coli. The new vectors have been designed to overcome certain drawbacks of the pComb3x plasmid. These new vectors include pRL5, pRL5-CAT, pRL5 asc-CAT and pRL5 bsi-CAT. This sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid; vector; replication; expression; foreign genetic; bacteria; cyanobacterium; Escherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT; pRL5-CAT; pRL5-CAT; gene; ds.
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/product= "Kappa constant region amino acid sequence"
4298..4363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                              Novel plasmid useful in cloning and expression of foreign genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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Pred. No. 6.5e-14;
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                                                                                                                                                              Mcwhirter J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6122 BP; 1449 A; 1571 C; 1639 G; 1463 T; 0 other;
                                                                                                                                                                                                                                       P-PSDB; AA022535, AA022536, AA022537, AA022538, AA022539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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/product= "CAT amino acid sequence"
                                                                                                                                                            Wild M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pRL5 bsi-CAT nucleic acid sequence.
                                                                                                                                                            Barbas-frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 7A-E; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL41115 standard; DNA; 6122
07-DEC-2001; 2001WO-US46516.
                                                    08-DEC-2000; 2000US-254411P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/product= "C
3947..4267
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                                                                                                       (ALEX-) ALEXION PHARM INC
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WO200246435-A2
                 misc_feature
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                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                          13-JUN-2002
                                                                    misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowdish KS,
                                           promoter
                                                                                              RBS
                                                                                                              SDS
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                                                                                                                                                                                                                                                                              SDS
                                                                                                                                                                                                                                                                                                                        SOS
  The invention relates to a plasmid with a nucleic acid sequence of 6122, or 5683 base pairs fully defined in the specification. The invention more specifically relates to novel vectors capable of replication and expression of foreign genetic information in bacteria, such as, for example, cyanobacterium and E. coli. The new vectors have new vectors include pRLS, pRLS, arc. CAT and pRLS bsi-CAT. This polymucleotide sequence represents the plasmid pRLS bsi-CAT nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                         3050 Arcaaaaadacadcrarceccarrecagrecacrecrecrecrrecraceracereccas 3109
                         /*tag= e
/product= "CH1, His6 tag, HA tag, and gene III amino acid
sequence"
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                                                                                                                                                                                                                                                                                                                                                                        ATGAAAAAAGACAATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTGGCCCAG
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                      Novel plasmid useful in cloning and expression of foreign genetic
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1013..1672
                                                                                                                                                                                                                                                                                                                                       DB 24; Length 6122;
/product= "pel B leader amino acid sequence"
5,779..6090
                                                                                                                                               Mcwhirter J;
                                                                                                                                                                                                                                                                                                                      Sequence 6122 BP; 1447 A; 1571 C; 1641 G; 1463 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                       P-PSDB; AA022535, AA022536, AA022538, AA022539, AA022541
                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 66; DB 24; Best Local Similarity 100.0%; Pred. No. 6.5e-14; Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                              Barbas-frederickson S, Wild M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pTL5-CAT; vector; antibody; gene; ds
                                                                                                                                                                                                                Disclosure; Fig 11A-E; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product= "Amp frag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN84078 standard; DNA; 6122 BP
                                                                                           07-DEC-2001; 2001WO-US46516
                                                                                                             08-DEC-2000; 2000US-254411P
                                                                                                                                                                                                                                                                                                      sequence of the invention.
                                                                                                                             (ALEX-) ALEXION PHARM INC.
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/partial
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                                                           WO200246436-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                              Bowdish KS,
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                                                                           13-JUN-2002
                                                                                                                                                                                                  information
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                 CDS
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Plasmid for in situ production of genes, comprises two template annealing sequences, such as downstream primer and upstream collar sequence and a restriction site located between the annealing sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin Y, Renshaw M, Wild M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            include a start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene= "Gene III"
'note= "the CDS does not include a start codon"
                                                                                                                                                                                                                                                                                                                                                              *tag= g
'partial'
'pactouct= "OmpA leader"
'note= "the CDS does not include a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "pelB leader"
/note= "the CDS does not include a stop codon"
4365..5147
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note= "light chain variable region stuffer"
951..4269
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/*tag= b
/product= "Chloramphenicol transferase"
complement (2052..2651)
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                                                                                                                                                       *tag= d
note= "lac promoter"
                                                                                                                                                                                                                                     *tag= e
note= "lac rep site"
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note= "Kappa Cns"
                                                                        *tag= c
note= "ori"
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1050.3115
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                         Plasmid, vector, replication, expression, foreign genetic, bacteria, cyanobacterium, Escherichia coli, pComb3X plasmid, pRL5, pRL5 asc-CAT, pRL5-CAT, pRL5 bsi-CAT, gene, ds.
                                                                                                                                                                              1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTTCGCTACCGTGGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence"
                                                                                                                                                            Gaps
      mRNA. The plasmids are engineered to contain 2 template annealing sequences (see ABN84079-80 and ABN84082-83), i.e. a downstream primer that anneals to a first portion of a nucleic acid template, e.g. mRNA encoding at least a portion of an antibody, an upstream collar sequence that anneals to a second portion of the template, and at least 1 restriction site located between the 2 template annealing sequences. A single-stranded DNA plasmid vector is produced containing a nucleic acid encoding at least a portion of a polypeptide, e.g. a light chain and/or a heavy chain of an antibody. This vector can be transformed into a host cell and
directly incorporated into the plasmid by reverse transcription of
                                                                                                                                                            °,
                                                                                                                                         DB 24; Length 6122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Kappa constant region amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Omp.A leader amino acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B leader amino acid sequence
                                                                                                                       Sequence 6122 BP; 1449 A; 1571 C; 1639 G; 1463 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barbas-frederickson S, Wild M, Mcwhirter J;
                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            "CAT amino acid sequence"
                                                                                                                                         Score 66; DB 24;
Pred. No. 6.5e-14;
                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                        Plasmid pRL5 CAT-Asc nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Cocation/Qualifiers
                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                         100.0%;
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/product= '
sequence"
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/product=
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                                                                                                                                                 Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                       16-OCT-2002
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                                                                                                                                                                                                                  61
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                                                                                                                                         Query Match
                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                RESULT 13
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The invention relates to a plasmid with a nucleic acid sequence of 6122, or 5683 base pairs fully defined in the specification. The invention more specifically relates to novel vectors capable of replication and expression of foreign genetic information in bacteria, such as, for example, cyanobacterium and E. coli. The new vectors have been designed to overcome certain drawbacks of the pcombix plasmid. These new vectors include pRLS, pRLS-CAT, pRLS asc-CAT and pRLS bai-CAT. This polynucleotide sequence represents the plasmid pRLS CAT-Asc nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120; 3b1; 3b4; 3b9; MA; MY4; humanised; monoclonal antibody; MAb; immunoreaction; neutralisation; passive immunotherapy; tetanus toxin; alkaline phosphatese; phoA; ss; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                              Novel plasmid useful in cloning and expression of foreign genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic human neutralising monoclonal antibodies to human immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-induced disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6125 BP; 1447 A; 1573 C; 1644 G; 1461 T; 0 other;
                          P-PSDB; AAO22535, AAO22536, AAO22538, AAO22539, AAO22540.
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                                                                                                                                                                  Claim 1; Fig 9A-E; 39pp; English
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Best Local Similarity 100.0%;

Matches 66; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of the invention.
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2002-537570/57
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modified version of the phagemid expression vector, promb3 given in AA092546. pho-TT provides for the expression of soluble Fabs which are secreted into the periplasmic space which is regulated from the alkaline phosphatase (phoA) promoter. This plasmid was used within the scope of the invention to express various mutagenised human Fab's which comprise heavy and light variable regions which bind to HIV gpl20. ppho-TT consists of a DNA molecule having two cassettes to express two soluble proteins a heavy chain and a light chain. The vector comprises, operatively linked 5' to 3', a first cassette consisting of the phoA promoter/operator sequences, an ECORI restriction site, a spacer region bridge site (RBS), an OmpA leader, a Sfil restriction site, a spacer region brordered by 5' saci and 3' XDaI restriction cassette consisting of an expression control RBS, a PelB leader, a human cassette consisting of an expression control RBS, a PelB leader, a human consenus amino terminus specer region comprising the sequence EVQLE.

Coloning region bordered by 5' XNoI and 3' SpaI restriction site.

Coloning region bordered by 5' XNoI and 3' SpaI restriction site.

Coloning region bordered by 5' XNoI and 3' SpaI restriction site.

Coloning region bordered by 5' XNoI and 3' SpaI restriction site.

Coloning region site. The pho-TT expression control stop sequences and a NoI restriction site.

Chain stuffer that is 1200 by in length and a heavy chain stuffer that is 1200 by in length and a heavy chain stuffer that is 1200 by in length and a heavy chain stuffer that is 1200 by in length and a heavy chain stuffer that is 1200 by in length and a heavy wail light chain stuffer seconds.
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1 ATGAAAAAGACAACTATCGCGATTGCAGTGGCACTGGCTTTCGCTACCGTGGCCCCAG
                                                                          0; Gaps
                                  Length 6166;
Sequence 6166 BP; 1416 A; 1706 C; 1629 G; 1415 T; 0 other;
                                                                      0; Indels
                                    Score 66; DB 16;
Pred. No. 6.5e-14;
                                  ch 100.0%; Score 66; DB
1 Similarity 100.0%; Pred. No. 6.5
66; Conservative 0; Mismatches
                                                     Best Local Similarity
                                      Query Match
                                                                      Matches
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4601 GCGGCC 4606 61 GCGGCC 66 ઠે

AAQ10569 standard; DNA; 73 BP AAQ10569; 

26-APR-1991 (first entry)

Omp A signal peptide-encoding sequence.

Mirabilis antiviral protein; MAP; Omp A signal sequence; ds.

Mirabilis jalapa.

EP414134-A

27-FEB-1991

90EP-0115718. 16-AUG-1990;

89JP-0210767. 17-AUG-1989; Tsuge H, Habuka N, Akiyama K,

WPI; 1991-059386/09.

(NISB ) JAPAN TOBACCO INC.

Matsumoto T,

Gene encoding Mirabilis Antiviral Protien and OmpA signal peptide for mass-prodn. of extracellular MAP

Claim 1; page 8; 15pp; English.

This Omp A signal peptide-encoding sequence is contained in a

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recombinant plasmid, flanked on its 3' side by a Mirabilis antiviral protein (MAP) gene. The plasmid is used to transform E.coli host cells in the large-scale prodn. of MAP. The 5' end overhangs the 3' end of the complementary strand by TA and the 5' end of the complementary strand by TA and the 5' end of the complementary strand by TA and the 5' end of the complementary strand by TA and this sense
                                                                                                                                                                 strand by CTAG. See also AAQ10568.
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Sequence 73 BP; 16 A; 20 C; 21 G; 16 T; 0 other;

Gaps .; 0 Length 73; 3; Indels Score 60.2; DB 12; Pred. No. 2.7e-12; 0; Mismatches 3; 91.2%; Query Match
Best Local Similarity 95.4
Matches 62; Conservative

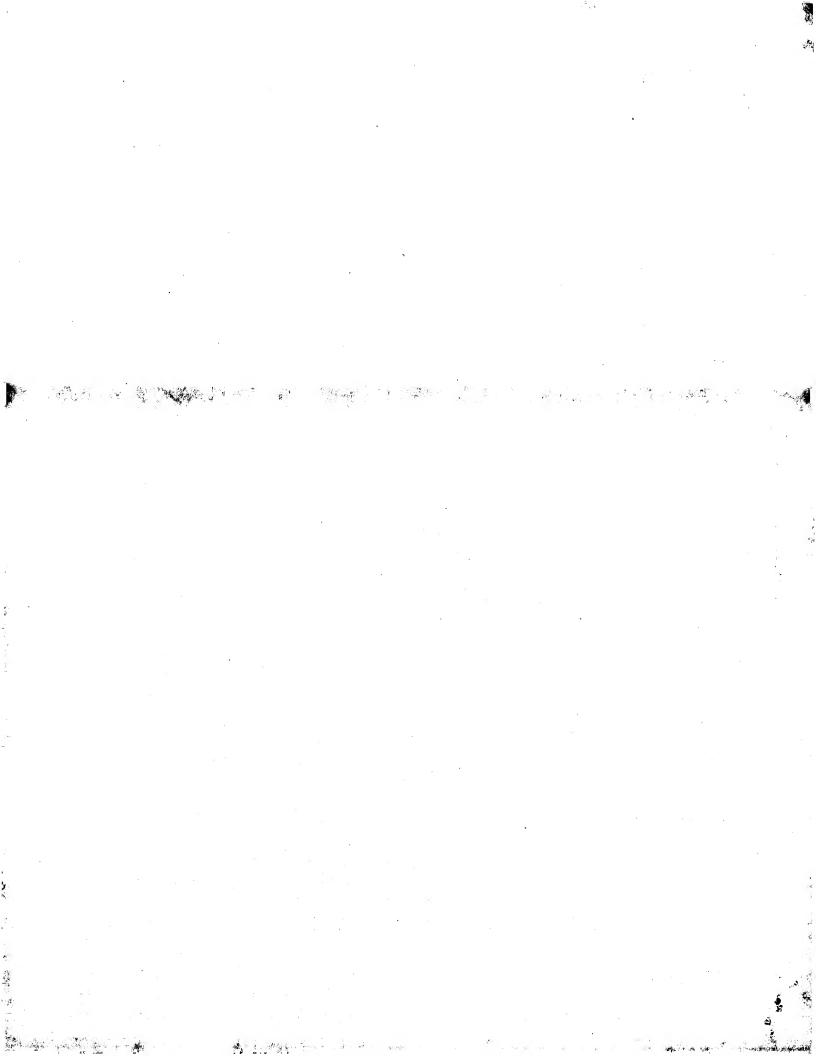
9 2 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGCTTTCGCTACCGTAGCGCAG 61 셤 ઠ

61 GCGGC 65

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99 25225

Search completed: August 18, 2003, 23:28:49 Job time : 24.2513 secs



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RESULT 2
US-08-591-632-43
Sequence 43, Application US/08591632
Sequence 43, Application US/08591632
Settle No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Righard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNOBFICIENCY VIRUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               US-09-318-786-20
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1, Appli
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                                                                            August 18, 2003, 22:51:23 ; Search time 5.16534 Seconds (without alignments) 5639.757 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51, A
Sequence 2, Ap
Sequence 10, A
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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                                                                                                                                                                                                                                                                                                                                                   /cgn2 6/ptodata/2/ina/5A COMB.seq:*
/cgn2 6/ptodata/2/ina/5B_COMB.seq:*
/cgn2 6/ptodata/2/ina/6A COMB.seq:*
/cgn2 6/ptodata/2/ina/6B_COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-591-632-43

US-08-591-632-51

US-08-11-451-51

US-09-611-451-51

US-09-611-451-51

US-08-666-354A-10

US-08-439-132-1

US-08-828-741B-1

US-09-10-299-1

US-09-10-299-10

US-09-10-299-10
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
                                                                                                                                                                         IDENTITY_NUC Gapop 10.0
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                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
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1490
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Match 1
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Perfect score:
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Maximum DB
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No.
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APPLICANT: Janda, Kim D
APPLICANT: Wirsching, Peter
APPLICANT: Wirsching, Peter
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Richard A
TAPLICANT: Gao, Changshou
TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON
TITLE OF INVENTION: PLIAMENTOUS PHAGE USING PVII AND DIX, COMPOSITIONS,
TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
FILE REFERENCE: TSR0305S
CURRENT APPLICATION NUMBER: US/09/318,786
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 3450
                                                         Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, A
Sequence 12,
Sequence 12,
                                                                                        Sequence 1, Sequence 3, Sequence 3, Sequence 1, Sequence 1, Sequence 5, Sequence 5, Sequence 7, Sequen
        Sequence 5,
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US-09-553-498-5
US-09-518-869-5
US-09-553-498-1
US-09-518-869-1
US-09-618-869-1
US-09-618-869-3
US-08-256-790-1
US-08-256-790-1
US-08-26-790-1
US-08-26-790-1
US-09-26-790-1
US-09-218-262-7
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US-09-218-262-7
US-09-218-262-7
US-09-218-238-6
US-09-218-238-6
US-09-218-238-6
US-09-218-238-6
US-09-218-238-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09318786; Patent No. 6472147; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 66; Conservative (
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(619) 784-9399
                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                  ZIP: 92037
COMPUTER READABLE FORM:
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Best Local Similarity 100...
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2671 GCGGCC 2676
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OPERATING SYSTEM:
SOFTWARE: Patentl
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Patent No. 6395275
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Burton, Dennis R.
Lerner, Righard A.
TITLE OF INVENTION: SYNTHEFFIC HUMAN NEUTRALIZING MONOCLONAL
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CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                    STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8 CITY: La Jolla
The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent Counsel
STREET: 10550 No. 6395275th Torrey Pines Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1e-13;
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100.0%; Pred. No. 1.1e-13
iive 0; Mismatches 0
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-CCT-1994
PRIOR APPLICATION DATE: 19-CCT-1994
FILING DATE: 19-CCT-1994
PRIOR APPLICATION NUMBER: PCT/US94/11907
PRIOR APPLICATION DATE: APPLICATION NUMBER: US 08/308,841
PRIOR APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-CCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSRI 332.3
                                                                                                                                                                                                               SOFTWARE: Patentin Release #1 CURRENT APPLICATION DATA:
                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (619) 784-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: CA
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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USA
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                                                                           STATE: C. COUNTRY:
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2611 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTGGTTTCGCTACCGTGGCCCAG 2670
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Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Barton, Dennis R.
APPLICANT: Lerner, Aighard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNOBEFICIENCY VIRUS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 66; DB 4; Length 4691; 100.0%; Pred. No. 1.1e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
                                                                                               PAPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-5EP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APPLICATION NUMBER: US 08/233,619
FILING DATE: 19-007-1993
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: (619) 784-293
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TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/OCKET NUMBER: 42
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 66; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703-205-8050
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Burton, Dennis R.
Lerner, Righard A.
TITLE OF INVENTION: SYNTHAND NEUTRALIZING MONOCLONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 66; DB 3; Length 6166; 100.0%; Pred. No. 1.2e-13; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IEM PC compatible
COMPARE: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-041-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
                                                                               PRIOR APPLICATION UNMER: PCT/US94/11907
PRIOR APPLICATION NUMBER: PCT/US94/11907
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fiting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 784-2937
TELEPAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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Gaps
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Pred. No. 1.2e-13;
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Fatent No. 5340732
GENERAL INFORMATION:
APPLICANT: HABUKA, No. 5340732iyuki
APPLICANT: MATSUMOTO, Takashi
APPLICANT: NOMA, Masana
TITLE OF INVENTION: AMTIVIRAL PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH, & BIRCH
STREET: 8110 Garchouse Road, Suite 500 East
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,845B
FILING DATE: 20-MAR-1992
CLASSIFICATION: 530
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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MOLECULA TYPE: DNA (genemic)
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-611-451-51
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1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCT
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                          61 GCGGC
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                                                                                                                                                                              US-08-439-132-1
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                                                                                                                                                                                                                                     Gaps
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APPLICANT: KRAMER, JOACHIM
APPLICANT: MEYER, THOMAS F.
APPLICANT: MEYER, THOMAS F.
APPLICANT: POHLARER, JOHANNES
TITLE OF INVENTION: BACTERIA USED TO PRODUCE STABLE FUSION
TITLE OF INVENTION: PROTEINS AND METHOD FOR THEIR IDENTIFICATION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                               Length 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUNTAIL: CONTROLL 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,354A
FILING DATE: 23-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "FRAGMENT OF PLASMID pJK165"
                                                                                                                                                                                                                                                                          ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP. STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                               Score 60.2; D
Pred. No. 4.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 147-157P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08666354A Patent No. 6040141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 base pairs
                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                             Query Match
Best Local Similarity 95.4%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.4
Matches 62; Conservative
SEQUENCE CHARACTERISTICS:
                      73 base pairs
                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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US-07-854-845B-2
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                  LENGTH:
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102 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTGGTTTCGCTACCGTAGCGCAG 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                     APPLICANT: Wong, W. K.R.
APPLICANT: Sutherland, Margaret L.
TITLE OF INVENTION: EXCRETION OF HETEROLOGOUS PROTEINS FROM
TITLE OF INVENTION: E.COLI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WONG, RAYMOND W.K.;SUTHERLAND, MARGARET L. IILLE OF INVENTION: EXCRETION OF HETEROLOGOUS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60.2; DB 1;
Pred. No. 6.2e-12;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE DOCKET NUMBER: 16777/200/ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5309
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,132
FILING DATE: 11-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM E.COLI
MUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/395,797
FILING DATE: 18-AUG-1989
                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street
CITY: Washington
Sequence 1, Application US/08439132; Patent No. 5646015; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 249 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.4'
Matches 62, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Patent No. 6043069

GENERAL INFORMATION:

APPLICANT: Koentgen, Frank
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.

TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
CUNTRY: United States of America
                                                                                                                                                                                                                                                             Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60.2; DB 3; Length 548;
Pred. No. 7.2e-12;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

SOFTWARE: DAGHIN BC COMPATION

APPLICATION DATA:

APPLICATION NUMBER: US/08/828,741B

FILING DATE: 26-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: DIGIGIO, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10591

TELEPHONE: (516) 742-4346

TELEPHONE: (516) 742-4366

TELEFAX: (516) 742-4366

TE
                                                                                                                                                                                                                                                      Score 60.2; DB 6;
Pred. No. 6.2e-12;
0; Mismatches 3;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 239,145
FILING DATE: 31-AUG-1988
                                                                                                                                                                                                                                                      91.2%;
95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.2%;
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Best Local Similarity 95.48
Matches 62, Conservative
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.4
Matches 62; Conservative
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                                                                                                                                               LENGTH: 249
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; LOCATION:
US-08-828-741B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-08-828-741B-1
                                                                                                      SEQ ID NO:1
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0; Gaps
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Sequence 1, Application US/09160567

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Trailinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60.2; DB 4; Length 548;
Pred. No. 7.2e-12;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PIPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILLING DATE:
PILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELEPHONE: (516) 742-4343
TELEPAX: 230 901 SANS UR
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York : United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 11530
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.4
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: CDS
; LOCATION: 1..548
US-09-160-567-1
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                                                             61 GCGGC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                           RESULT 11
US-09-160-567-1
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RESULT 12

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Cells Carrying The Phagemids, A
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STRANDEDNESS: single strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 base pairs
                                                                                                                                                                                                                                                                             ZIP: 10017-4059
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                     New York
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) IMMEDIATE SOURCE:
US-08-880-829-21
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CELL TYPE:
CELL LINE:
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                                                                                                                                                                                                                                     STATE: Ne COUNTRY:
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               Sequence 1, Application US/09710299
Patent No. 6521741
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
Suess, Gabriele M.
Tarlinton, David M.
Treutlein, Herbert R.
Treutlein, Herbert R.
PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.2%; Score 60.2; DB 4; Length 548; Best Local Similarity 95.4%; Préd. No. 7.2e-12; Matches 62; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/710,299
FILING DATE: 09-No. 6521741-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/08880829
Patent No. 5925559
GENERAL INFORMATION:
APPLICANT: Collins, John
APPLICANT: Roettgen, Peter
TITLE OF INVENTION: A Collection of Phagemids, A
TITLE OF INVENTION: Collection of Escherichia Coli
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
RDDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America ZIP: 11530
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: DIG12140, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEFHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DUCATION: 1.548

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-710-299-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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US-08-880-829-21
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US-09-710-299-1
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Gaps
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                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM-XT COMPATIBLE
COMPUTER: IBM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3:
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,829
FILING DATE: 23-JUN-1997
CLASSIFICATION DATE: 23-JUN-1997
CLASSIFICATION DATE: 06/02/95
PRIOR APPLICATION DATE: 06/02/95
FILING DATE: 06/02/94
ATTORNEY/ACATION NUMBER: GERMAN DE P 94 108 689.4
FILING DATE: 06/07/94
ATTORNEY/ACATION NUMBER: 25,331
REGISTRATION NUMBER: 25,331
REGISTRATION NUMBER: 25,331
REGISTRATION NUMBER: 2272-77
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 682-3485
TELERAX: (212) 682-3485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.3%; Score 59.6; DB 2; Best Local Similarity 93.9%; Pred. No. 1.1e-11; Matches 62; Conservative 0; Mismatches 4;
                     NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joseph T. Eisele
ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,
ADDRESSEE: Levy, Eisele and Richard
STREET: 711 Third Avenue
CITY: New York
And Phagemid Particles
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RESULT 14

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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
3: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: August 19, 2003, 08:35:08 Job time : 7.16534 secs
                                                                                  New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DiGIGLIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4346
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.3%;
Best Local Similarity 93.9%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                              STREET: 400 Garder
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..470
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                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
US-09-160-567-10
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                                                                                                  APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: ACCOUNT MANAGERS.
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59.6; DB 3; Length 470;
Pred. No. 1.1e-11;
0; Mismatches 4; Indels
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APPLICANT: Koentgen, Frank
APPLICANT: Suese, Gabriele M.
APPLICANT: Suese, Gabriele M.
APPLICANT: Treutlein, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: ILESA

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: TEM PC compatible

COMPUTER: TEM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828,741B

FILING DATE: 26 MAR-1997

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:

NAME: DIGIGLIO, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10591

TELEPHONE: (516) 742-4366

TELEFA: (516) 742-4366

TELEFA: (516) 742-4366

TELEFA: (516) 742-4366

TELEFA: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 470 base pairs

TYPE: MUCLEIC CASINGEN

TO BENGTH: A 70 base pairs

TYPE: MUCLEIC CASINGEN

TO BENGTH: A 70 base pairs

TYPE: MUCLEIC CASINGEN

TO BENGTH: A 70 base pairs

TYPE: MUCLEIC CASINGEN

TO BENGTH: A 70 base pairs

TYPE: MUCLEIC CASINGEN

TO BENGTH: A 70 base pairs

TYPE: MUCLEIC CASINGEN

TO BENGTH: A 70 base pairs

TO BENGTH: A 70 base pairs
               Sequence 10, Application US/08828741B Patent No. 6043069
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Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.3%;
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Best Local Similarity 93.9
Matches 62; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-828-741B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-160-567-10
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Gaps

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DB 4; Length 470; 4; Indels

Score 59.6; DB 4; Pred. No. 1.1e-11; 0; Mismatches 4

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Copyright (c) 1993 - 2003 Compugen Ltd.
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August 19, 2003, 04:46:44; Search time 18.6243 Seconds (without alignments) 7930.701 Million cell updates/sec
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OM nucleic - nucleic search, using sw model
                                                                                                                              US-09-987-455
                                          Run on:
                                                                                                                          Title:
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Perfect score:	66
Sequence:	1 atgaaaagacagctatcgcctaccgtggcccaggcgg
Scoring table: IDENTITY NUC	1DENTITY NUC
Gapop 10.0 ,	Gapop 10.0 , Gapext 1.0

3008958	
parameters:	
chosen	
satisfying	
hits	
of	
number	
Total	

1504479 seqs, 1118970152 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%	Match 100	DISCING LIEST 45 SUMMATIES
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Published Applications NA:* 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*	2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*	<pre>4: /cgnz_b/ptodata/2/pubpna/USU6_NEW_FUB.8eq:* 4: /cgn2_6/ntodata/2/mihnna/USU6_PUBCOMR_seq:*</pre>			7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seg:*	8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*	9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:	10: /cgn2 6/ptodata/2/pubpna/US09B PUBCOMB.seq	11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq	<pre>12: /cgn2_6/ptodata/2/pubpna/US09 NEW PUB.seq:</pre>	13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq	14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq	15: /cgn2_6/ptodata/2/pubpna/US10 NEW PUB.seq:	<pre>16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:</pre>	<pre>17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seg:*</pre>
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Database															
	: Pub]	: Pub] 1: ,	: Published 1: /cgn2_ 2: /cgn2_ 3: /cgn2_ 4: /cgn2_	: Published 1: /cgn2_ 2: /cgn2_ 3: /cgn2_ 4: /cgn2_ 5: /cgn2_	: Published 1: /cgn2_ 2: /cgn2_ 3: /cgn2_ 4: /cgn2_ 5: /cgn2_ 6: /cgn2_	. Published 1: /cgn2 2: /cgn2 3: /cgn2 4: /cgn2 5: /cgn2 7: /cgn2	Published 1: /cgn2 2: /cgn2 3: /cgn2 4: /cgn2 5: /cgn2 6: /cgn2 7: /cgn2	: Publishe   1: /cgn2   2: 2: 2: 2: 2: 2: 2: 2: 2: 2: 2: 2: 2:	Publi	Publi	Publi	Publi	Publi	Publi	Publication of the property

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli	Sequence 6, Appli	Sequence 2, Appli Sequence 5, Appli	9	Sequence 1, Appli	Sequence 1, Appli	10,	Sequence 7, Appli	Sequence 39, Appl	Sequence 5, Appli	Sequence 15, Appl	e,	Sequence 38, Appl	Sequence 40, Appl
SUMMARIES	1 US-09-987-457-1	1 US-09-987-455-6	1 US-09-987-455-2 1 US-09-987-455-5	4 US-10-006-593-60	4 US-10-006-591-1	2 US-10-345-618-1	2 US-10-345-618-10	2 US-10-345-618-7	US-09-809-517A-39	2 US-10-345-618-5	2 US-10-345-618-15	2 US-10-345-618-3	US-09-809-517A-38	US-09-809-517A-40
% Query Match Length DB	66 1	66 1	1128 1	5149 1	6122 1	548 1	470 1	599 1	932 9	1031 1	1479 1	1490 1	1574 9	4425 9
% Query Match	100.0	100.0	100.0	100.0	100.0	91.2	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3
Score	99	9 0	99	99	99	60.2	59.6	59.6	59.6	59.6	59.6	59.6	59.6	29.6
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Sequence 36, Appl Sequence 41, Appl Sequence 41, Appl Sequence 4, Appli Sequence 3, Appli Sequence 13, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 30, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 37, Appl Sequence 11, Appl
US-10-001-934-36 US-10-001-934-36 US-09-80-517A-41 US-09-16-517A-41 US-09-16-29-4 US-09-848-616-8 US-09-848-616-8 US-09-916-230-13 US-09-912-165-18 US-09-912-195-396-3 US-09-912-396-3 US-09-912-397-18 US-09-782-397-13 US-09-782-397-13 US-09-782-397-13
44 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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## ALIGNMENTS

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Sequence 1, Application US/09987457

Sequence 1, Application US/09987457

Sequence 1, Application No. US2003001315041

GENERAL INFORMATION:

APPLICANT: Manosroi, Jiradej

APPLICANT: Manosroi, Jiradej

APPLICANT: Tayapiwatana, Chatchai

APPLICANT: Tayapiwatana, Chatchai

APPLICANT: Tayapiwatana, Chatchai

APPLICANT: Tayapiwatana, Chatchai

APPLICANT: Werner, Rolf-Guenther

TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes

FILE REFERENCE: 0652.180001

CURRENT APPLICATION NUMBER: US/09/987,457

CURRENT FILING DATE: 2001-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LEMOTH: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
; ORGANISM: Escherichia coli
US-09-987-457-1
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                                                                                                                                                        Sequence 2, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                 61 GCGGCC 66
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                                                    | FUDLICALION NO. USZU030049729A1
| GENERAL INFORMATION:
| APPLICANT: Aranya Manosroi
| APPLICANT: Jiradej Manosroi
| APPLICANT: Chatchai Tayapiwatana
| APPLICANT: Chatchai Tayapiwatana
| APPLICANT: Friedrich Goetz
| APPLICANT: Friedrich Goetz
| APPLICANT: Rolf-Guenther Werner
| TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
| TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
| TITLE OF INVENTION: Man-Derived tPA or K2S Molecules
| FILE REFERENCE: 0652.2190001
| CURRENT APPLICATION NUMBER: US/09/987,455
| CURRENT PELLING DATE: 2001-11.14
| PRIOR PILING DATE: 2001-11.14
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 3
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                               Sequence 3, Application US/09987455 Publication No. US20030049729A1
                                                  US20030049729A
                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Escherichia coli
US-09-987-455-3
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US-09-987-455-6
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LENGTH: 66
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APPLICANT: Aranya Manosroi
APPLICANT: Aranya Manosroi
APPLICANT: Chatchal Tayapiwatana
APPLICANT: Chatchal Tayapiwatana
APPLICANT: Chatchal Tayapiwatana
APPLICANT: Chatchal Tayapiwatana
APPLICANT: Chatchal Goetz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Mothods for Large Scale Production of Recombinant
TITLE OF INVENTION: Mothods for Large Scale Production of Recombinant
TITLE OF INVENTION: Mothods for Large Scale Production of Recombinant
TITLE OF INVENTION: Mothods for Large Scale Production of Recombinant
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH, 1128
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APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Mobile 1004,0001
CURRENT FILING DATE: 2001-11-14
PRIOR PAPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 25
SEQ ID NOS: 25
LENGTHER: Patentin Ver. 2.1
SEQ ID NO 5
LENGTHER: LENGTH: 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: coding; OTHER INFORMATION: sequence for OmpA-K2S fusion protein US-09-987-455-2
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APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REPERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT PILING DATE: 2003-01-16
PRIOR PILING DATE: 2000-06-09
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OTHER INFORMATION: Description of Artificial Sequence:LHL nucleotide
OTHER INFORMATION: sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 6122;
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; OTHER INFORMATION: Description of Artificial Sequence: vector
US-10-006-591-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 14;
Pred. No. 1.5e-15;
; Mismatches 0;
                                   CURRENT APPLICATION NUMBER: US/10/006,591
CURRENT FILING DATE: 2001.12-05
PRIOR APPLICATION NUMBER: 60/251,440
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
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; Publication No. US20030148484A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10345618
Publication No. US20030148484A1
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Best Local Similarity 100.0%;
Matches 66; Conservative 0
                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 16
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Best Local Similarity
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US-10-345-618-10
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APPLICANT: Renshaw, Mark
APPLICANT: Wild, Martha
APPLICANT: Mild, Martha
APPLICANT: Mild, Martha
APPLICANT: McWhirter, John
TITLE OF INVENTION: ENGINEERED FLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                            Length 1128;
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                                                                                            OTHER INFORMATION: Description of Artificial Sequence: coding OTHER INFORMATION: sequence for OmpA-K2S fusion protein US-09-987-455-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
   APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
   APPLICANT: Frederickson, Shana
   APPLICANT: Renshaw, Mark
   TILE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
   FILE REFERENCE: 1087-2
   CURRENT APPLICATION NUMBER: US/10/006,593
   CURRENT FILING DATE: 2001-12-05
   PRIOR PELICATION NUMBER: US 60/281,448
   PRIOR PELICATION NUMBER: US 60/281,488
   PRIOR PELICATION NUMBER: US 60/284,068
   PRIOR FILING DATE: 2001-05-04
   PRIOR FILING DATE: 2001-05-29
   NUMBER OF SEQ ID NOS: 118
   SOFTWARE: PatentIn version 3.1
   SEQ ID NO 60
   LENGTH: 5149
   LUMBER: CANDERS OF 
                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 66; DB 11; Best Local Similarity 100.0%; Pred. No. 9.7e-16; Matches 66; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.5e-15;
ive 0; Mismatches 0;
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APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shana
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: artificial sequence
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Best Local Similarity 100.0
Matches 66; Conservative
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US-10-006-593-60
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APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
                                APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 470;
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LOCATION: (1)..(597)
OTHER INFORMATION: Description of Artificial Sequence:LHL.seq
OTHER INFORMATION: nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(468)
OTHER INFORMATION: Description of Artificial Sequence:Kappa OTHER INFORMATION: nucleotide sequence
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Pred. No. 2.3e-13;
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                                                                                                                     FILE REFERENCE: 13474

CURRENT APPLICATION NUMBER: US/10/345,618

CURRENT FILING DATE: 2003-01-16

PRIOR APPLICATION NUMBER: US/09/509,031

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver: 2.1
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Publication No. US20030148484A1
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 93.9%;
Matches 62; Conservative
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ORGANISM: Artificial Sequence
                  Frank
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hes 62; Conserv
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                                                                                                                                                                                                                                                                                 SEQ ID NO 10
LENGTH: 470
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LENGTH: 599
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Best Local S:
Matches 62
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APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733Alel methods for displaying (poly) peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR PILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 39
LENGTH: 932
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APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REPERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT PILING DATE: 2003-01-16
PRIOR FILING DATE: 2000-06-09
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LOCATION: (1)..(1029)
OTHER INFORMATION: Beguence
OTHER INFORMATION: sequence
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Pred. No. 2.9e-13;
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                                                                                                                                                    Sequence 39, Application US/09809517A Patent No. US20020034733A1 GENERAL INFORMATION:
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Publication No. US20030148484A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: artificial sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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Best Local Similarity
                                          61 GCCGAC 66
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61 GCGGCC
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APPLICANT: Roentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herber R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
FILE REPERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO S: 16
                                                                     28 ATGABABAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCGG 87
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Publication No. US20030148484A1
Publication No. US20030148484A1
Publication No. US2003014848A1
APPLICANT: Koentgen, Frank
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: COMTLGL OTHER INFORMATION: nucleotide sequence
  4; Indels
  0; Mismatches
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CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
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Publication No. US20030148484A1
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LENGTH: 1490
TYPE: DNA
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
62; Conservative
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Matches
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GENERAL INFORMATION

APPLICANT: Lohning, Corinna

APPLICANT: Lohning, Corinna

TITLE OF INVENTION: No. US20020034733A1e1 methods for displaying (poly) peptides/prote

TITLE OF INVENTION: particles via disulfide bonds

TITLE OF INVENTION: particles via disulfide bonds

FILE REPERENCE: MORPHO/11

CURRENT PAPLICATION NUMBER: US/09/809,517A

CURRENT FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: EP 99114072.4

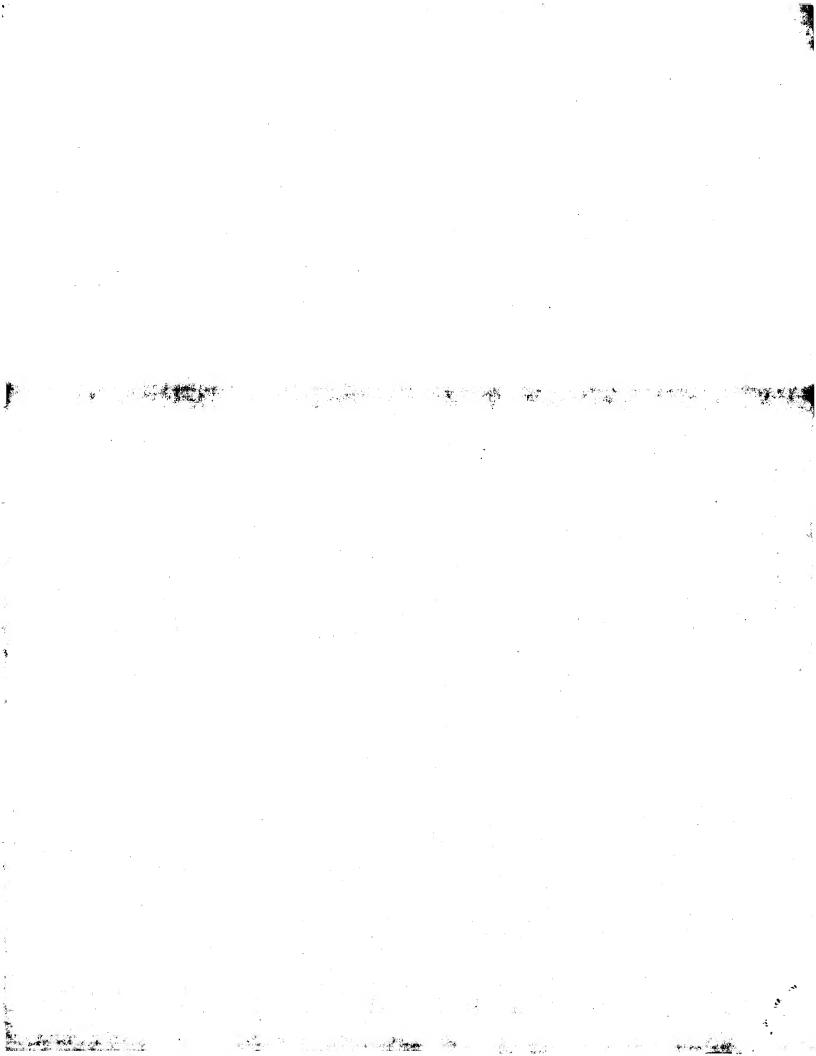
PRIOR PILING DATE: 1999-07-20

PRIOR PILING DATE: 2000-02-18

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.0

SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression cassette
US-09-809-517A-38
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; LOCATION: (1)..(1488)
; OTHER INFORMATION: Description of Artificial Sequence: CATAB-TEV
; OTHER INFORMATION: nucleotide sequence
US-10-345-618-3
                                                                                                                            Length 1490;
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Pred. No. 3.2e-13;
0; Mismatches 4;
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Job time : 19.6243 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/09809517A Patent No. US200200034733A1
                                                                                                                            Query Match
Best Local Similarity 93.9%;
Matches 62; Conservative
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Best Local Similarity 93.9%;
Matches 62; Conservative
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Perfect score:

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AA398159 Zt60e09.B
AA401699 Zt60e09.r
BY641012 BY641012
BU78334 in02g05.y
BU78334 in02g05.y
BU78331 TETRACOON
BI560274 60325391
BU853590 AGENCOURT
AQ90515 GSSTC0708
AU244728 AU244728
AU244560 AU244560
BGC34261 AGENCOURT
AQ90458 GSSTC0415
BQ40448 NISC_mp09
CA808042 CA1ZLIO11
CB3972 CARZSGOO0
BQ737333 AGENCOURT
BQ737331 AGENCOURT
CD101043 AGENCOURT
CB206099 AGENCOURT
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BQ094120 aan14204.
CD355744 UI-M-FYO-
BQ938965 AGENCOURT
AQ833659 HS 5261 A
AL260159 TETEAGGON
AL292142 TETEAGGON
AL215785 TETEAGGON
BES57231 pace1-60
H33495 EST109553 R
CA377775 656425 NC
CA373964 648233 NC
AL66295 AL966295
AL64617 AL644617
AL655729 AL655729
CA369617 646050 NC
AL636961 AL635729
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BE503913 hz35e09.x
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Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceee; Salmonella.
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Wong,R.M.-Y., Wong,K.K., Benson,N.R. and McClelland,M.
Wang,R.M.-Y., Wong,K. Benson,N.R. and McClelland,M.
Sample sequencing of a Salmonella typhimurium LT2 lambda library:
comparison to the Escherichia coli Kl2 genome
FEMS Microbiol. Lett. 173 (2), 411-423 (1999)
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Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifeci.sdsu.edu
Class: shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                         BU783334
BX099533
CNS099533
CNS099539
AU24728
AU244560
BQ34261
BQ34261
BQ731326
BQ600448
CCB366058
CCB366059
CCB101043
CD101043
AU184837
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CD355744
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CNS03TQE
CNS04IET
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AF075794.1 GI:3320664
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VERSION
KEYWORDS
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AUTHORS
TITLE
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CB806580 AMGNNUC:S
AI635506 ts95803.x
AW004057 wq85e09.x
                                                                                                     Search time 193.082 Seconds
(without alignments)
8307.845 Million cell updates/sec
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- 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srpg2-00054-g9"
/tissue type="srpg2 (10238)"
/clone_lib="srpg2 (10238)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; peneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB806580 386 bp mRNA linear EST 16-MAY-2003 AMGNNUC:SRPG2-00054-G9-A srpg2 (10238) Rattus norvegicus cDNA clone srpg2-00054-g9 5', mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/organism="Salmonella typhimurium"
/mol_type="genomic DNA"
/strain="LT2"
/db_xracn:602"
/clone="10"-T3"
/clone lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
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Plate: 00054 row: g column: 9.
Location/Qualifiers
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Pred. No. 8.9e-06;
1; Mismatches 8; Indels
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Pred. No. 48;
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RESULT 3

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Contact: Robert Strausberg, Ph.D.

Email: Gapabs-ramail.nih.gov

Tisgaue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-blo.llnl.gov/bbrp/image/image.html

Insert Length: 383 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers
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/lab host="DBLDB"
/clone_lib="NCI CGAP_GC6"
/clone_lib="NCI CGAP_GC6"
/note="Vector: pT7135-pac (Pharmacia) with a modified
/note="Vector: pT7135-pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258611, 1469064-1470993, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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AIG35506 310 bp mRNA linear : EST 14-DEC-1999
t895a03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238988 3',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 310)

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                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                 AI635506.1 GI:4686836
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Homo sapiens
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KEYWORDS
SOURCE
ORGANISM
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R. Emmert-Buck, M.D., Ph.D.
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Best Local
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AA398159/c
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not_1; Site_2: Eco R1; Plaamid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
teaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1228631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                       CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/limage/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 312)

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NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTTTCGCTACCGTGGCCCAGGCGG
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Pred. No. 97;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue type="pooled germ cell tumors"
lab host="DH108"
                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'clone="IMAGE:2478856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
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BE503913.1 GI:9706321
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1 Similarity 64.5%;
40; Conservative
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Unpublished
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Best Local Similarity
Matches 40; Conserv
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ORGANISM
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BES03913/c
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/clone="Interface | Caronis 1900 | /clone="Interface | Caronis 1900 | /clone="Interface | Caronis 1900 | /clone | Liberation | /clone | Caronis | Caroni
                           CONA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLone distribution: NG-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLML, send email to: info@image.llnl.gov.
Seq primer: -400P. from Gibco
High quality sequence stop: 313.
Location/Qualifiers
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1 (Dases 1 to 325)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Sreptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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zt60e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726760
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 392 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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AA398159
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                           40; Conservative
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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12466851
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                                                                                                                                                                                                                                                                                                   Query Match
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BY641012/c
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ORGANISM
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KEYWORDS
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1 (bases 1 to 340)

1 Hillar, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, Y., Waterston, R. and Wilson, R.
                                                                                                                                                                             /clome_llb="Soares_testis_NHT"
//note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from clontech Laboratories
                                                                                                                                                                                                                                                                                               Double-stranded cDNA was ligated to Ecc RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Ecc RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Patima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zt60e09.rl Soares_testis_NHT Homo saplens cDNA clone IMAGE:726760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 AAAAAACAGCCATCACCAGGCCATTCACGCTTTTGTTTAGCAGAGCCCAGGCAG 223
                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 392 Std Brror: 0.00
Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTGGCCCAGGCGG
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 40.6%; Score 26.8; DB 9; Length 325; Similarity 64.5%; Pred. No. 98; 40; Conservative 0; Mismatches 22; Indels
                  1. .325
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5923670"
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/clone="IMAGE:726760"
/sex="male"
                                                                                                 'db_xref="taxon:9606"
                                                                                                                   /clone="IMAGE:726760"
Location/Qualifiers
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                                                                                                                                                           'lab host="DH10B"
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72 c
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셤 ઠે 원

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmania; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Bukaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Mus. CB (kazaki,Y.; Furuno,M.; Kasukawa,T.; Adachi,J.; Bono,H.; Kondo,S.; Nikaido,I.; Osato,N.; Saito,R.; Suzuki,H.; Yamanaka,I.; Kiyosawa,H.; Yagi,K.; Tomaru,Y.; Hasegawa,Y.; Nogami,A.; Schonbach,C.; Corbani,J.B.; Baldarelli,R.; Hill,D.P.; Bult,C.; Hume,D.A.; Golobori,T.; Baldarelli,R.; Hill,D.P.; Bult,C.; Hume,D.A.; Dallak,B.; Dallak,B.; Darusic,V.; Chothia,C.; Corbani,J.E.; Cousins,S.; Dallak,E.; Dragani,T.A.; Fletcher,C.F.; Forrest, A.; Frazer,K.S.; Gasterland,T.; Gariboldi,M.; Gissi,C.; Godzik,A.; Gough,J.; Grimmond,S.; Gustincich,S.; Hirokawa,N.; Jackson,I.J.; King,B.L.; Konagaya,A.; Kurochkin,I.V.; Lee,Y.; Lenhard,B.; Lyons,P.A.; Magabhian,T.; Numata,K.; Okido,T.; Pavan,W.J.; Pertea,G.; Perteosky,N.; Pillai,R.; Pontius,J.U.; Mixinganian,T.; Numata,K.; Okido,T.; Pavan,W.J.; Pertea,G.; Percosky,N.; Pillai,R.; Pontius,J.U.; Reid,J.; Ringwald,M.; Sandelin,A.; Schneider,C.; Semple,C.A.; Setou,M.; Shimada,K.; Sultana,R.; Wagner,L.; Wahlestedt,C.; Wangy,Y.; Taylor,M.S.; Tasadale,R.; Naranabe,Y.; Wangle,Y.; Taylor,M.S.; Tasadale,M.; Sakazume,N.; Sato,K.; Shiraki,T.; Waki,K.; Kawai,J.; Aizawa,K.; Arakwa,T.; Fukuda,S.; Hara,A.; Hashizume,M.; Zarolan,K.; Sakai,K.; Sakai,B.; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 bp mRNA linear EST 15-DEC-2002 CDNA clone K430341N20 3', mRNA sequence.
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64.5%; Pred. No. 1e+02;
tive 0; Mismatches 22; Indels
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Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                       Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                    MA 02138
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                                                                                                                                                                                                                                                                                                                                                               Human Genome Sequences Mann. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues.

Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) Whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                                                                                                                    Email: genome-reaggsc.riken.go.jp,

Wil.http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Submission
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                                                                      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'clone="nescriber"
/tissue type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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                    Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/strain="C57BL/6J"
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Homo sapiens
                                                                                           Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Conservative
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l (bases 1 to 569)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Melton, D., Brown, J., Kenty, G., Permutt, A., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Badocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas BST project library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX099539 667 bp mRNA linear EST 06-FEB-2003
BX099539 Soares testis NHT Homo sapiens CDNA clone IMAGp998G231928
; IMAGE:782638, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: pancreas; Vector: pBluescript SK-; Site_1: MADI, Site_2: BCORI; Constructed with lambda ZABII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 AAAAAACAGCCATCACCAGGCCATTCACGCTTTGTGCTTTGTTAGCAGAGCCCAGGCAG 312
                                                                                                                                                                                                                                                                                                                                                                                                Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 429.
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                                                                                                                                                                                                                                                                                                                                  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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/tiseue type="insulinoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 64.5%;
Matches 40; Conservative
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us-09-987-455-3.rst

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- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                    Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Banil: cgapBs-ræmail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninot (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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/note="Genoscope sequence ID : COBG127CB06SP1-end
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                            provided by
                                               using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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/db_xref="taxon:99883"
/clone="127D11"
                            Estimate of human gene number
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      and Weissenbach, J.
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free from RZPD; contact RZPD; conteact RZPD (chone@rzpd.de) for further information. Seg primer: M13r, Primer seguence: TTTACACAGGAAACAGCTATGAC. Location/Qualifiers
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    Neubert, P., Partsch, E., Peters, M.,
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                                                                                Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD, IWAGP998G21928.
RZPDLIB; I.M.A.G.B. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
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Pred. No. 1.2e+02;
0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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Ebert, L., Heil, O., Hennig, S., Neuber
Radelof, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3
Unpublished
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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871 bp mRNA linear EST 16-OCT-2002
AGENCOURT 10418173 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6620518
5', mRNA Sequence.
BU853590.1 GI:24038556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2870 row: 1 column: 22
High quality sequence stop: 454.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 871)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (Dasts t. C. 8.1.)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov
Plate: LIAM1748 row f column: 03
High quality sequence stop: 772.
Location/Qualifiers
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40.6%; Score 26.8; DB 12; Length 786;
cal Similarity 64.5%; Pred. No. 1.3e+02;
40; Conservative 0; Mismatches 22; Indels 0;
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/db_xref="taxon:9606"
/clone="IMAGE:6620518"
/lab_host="DH108" (T1 phage-resistant)"
/clone_lib="NIH MGC_82"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Homo sapiens"
                                                                                                                                                'organism="Homo sapiens"
                                                                                                                                                                                                       clone="IMAGE:5295746"
                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="epimastigote"
/clone_lib="Trypanosoma cruzi random genomic library"
/clone_lib="Trypanosoma cruzi random genomic library"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphoryated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 09-JAN-2001
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Trypanosoma; Schizotrypanum.

I (bases 1 to 268)

Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.

A random sequencing approach for the analysis of the trypanosoma cruzi general structure, large gene and repetitive DNA families, and gene dan depetitive DNA families, and gene dand secovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSSTC07088 Trypanosoma cruzi random genomic library Trypanosoma cruzi genomic clone G55P8, genomic survey sequence. AQ905715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AAAAGACAGCTATCGCGATTGCAGTGGCACTGGTTTCGCTACCGTGGCCCAGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 871;
                                                                                                                                                                                                                                                                                                                                                                                                                                          40.6%; Score 26.8; DB 13; 64.5%; Pred. No. 1.4e+02;
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Fax: (54-11) 4752-9639
Email: dsanchez@iib.unsam.edu.ar
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/clone="G55P8"
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/dev_stage="late gastrula to early neurula stages 12.5-13"
/clone_lib="Shibata Xenopus AEM lambda-ZAP II cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 359)
Shibata,M., Itoh,M., Ohmori,S., Shinga,J. and Taira,M.
Systematic screening and expression analysis of the head organizer
genes in Xenopus embryos
Dev. Biol. 239 (2), 241-256 (2001)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Kenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan Science and Technology Corporation, Japan
T-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Email: m_taira@biol:s.u-tokyo.ac.jp,
URL:http://www.biol:s.u-tokyo.ac.jp,
Location/Qualifiers
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0
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                                                                                    Query Match 40.3%; Score 26.6; DB 28; Length 268; Best Local Similarity 71.4%; Pred. No. 1.1e+02; Matches 35; Conservative 0; Mismatches 14; Indels 0.
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Xenopus laevis
HincII site of the vector"
a 63 c 84 g 61
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/mol_type="mRNA"
/db_xref="taxon:8355"
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g
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Search completed: August 19, 2003, 08:29:16 Job time : 201.082 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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ing sw model	August 18, 2003, 19:53:48; Search time 4736.31 Seconds (without alignments)
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OM nucleic - nucleic search, using sw model	Run on:

(Without allymments) 9743.047 Million cell updates/sec	5-5	l atgaaaaagacagctatcgcttcgtgacaacatgcgaccg 1128
	US-09-987-455-5 1128	l atgaaaaagac
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2888711 segs, 20454813386 residues Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0 Searched:

5777422

Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

PAT 28-JUN-2002							. and Manosroi, J.	dna-derived tpa		
linear							, Manosroi, A	recombinant		
DNA							Ja, C.	of 1		;
AX431268 1128 bp		AX431268.1 GI:21656150	synthetic construct	synthetic construct	artificial sequences.	_	Goetz, F., Werner, R.G., Tayapiwatana, C., Manosroi, A. and Manosroi, J.	Methods for large scale production of recombinant dna-derived tpa	or k2s molecules	Patent: WO 0240650-A 2 23-MAY-2002;
RESULT 1 AX431268 LOCUS	DEFINITION ACCESSION	VERSION KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE		JOURNAL

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Patent: WO 0240650-A 5 23-MAY-2002;
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tive 0; Mismatches 0;
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/mol_type="genomic DNA"
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Pred. No. 5.5e-259;
Mismatches 0; Indels
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Corganism="synthetic cons/mol_type="genomic DNA"

db_xref="taxon:32630"
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ORIGIN  Query Match  Best Local Similarity 99.5%; Pred. No. 6.5e-244;  Matches 1068; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	aaaacagtgactgctactttgggaatgggtcagcctacgt6 11 	QY         116 GCACGCACAGCCTCACCGAGTGCGTCCTGCCTCCCGTGGAATTCCATGATCCTGA         175           DD         299 GCACGCACACCCTCACCGAGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA         358°	QY         176         TAGGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA         235           Db         359         TAGGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA         418	QY         236         ATTACTGCCGGAATCCTGATGGCCAAGCCCTGGTGCCACGTGCTAGAGAACCGCA         295           Db         419         ATTACTGCCGGAATCCTGATGGCGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCA         478	QY         296         GGCTGACGTGAGAGTACTGTGATGTGCCCTCCTGCTCCACCTGAGACAGTACA         355	Qy         356         GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC         415	Qy         416         AGGCTGCCATCTTTGCCAAGCACACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCA         475           Db         599         AGGCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCA         658	Qy         476 TACTCATCAGCTCCTGCTGGATTCTCTCTCGCCCACTGCTTCCAGGAGGTTTCCGC 535	QY         536         CCCACCACCACCAGAACTTAGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC         595	Oy 596 AGAAATTTGAAGAAAAATACATTGTCCATAAGGAATTCGATGATGACCACTTACGACA 655	Qy         656         AIGACATTGGGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCG         715           Db         839         AIGACATTGCGCTGCTGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCG         898	Oy 716 TGGTCCGCACTGTGCCTTCCCCCGCGGACCTGCAGCTGCAGCTGCAGCTGGAGTGTG 775	Qy 836 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATTTACTTAACAGAA 895	QY         896         CAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCCCCAGGCAAACT         955           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         956         TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA         1015	Oy 1016 TGACTTTGGTGGGCATCATCAGGTGGGGCCTGGGACAGAAGGATGTCCCGGGTG 1075
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AJUS93 1341 bp DNA linear PAT 04-AUG-1995
DNA for tissue plasminogen activator (t-PA) from patent EP0400545.
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CCCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCTGGCGAGGAGGAGC
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1 (bases 1 to 1341)
Stern,A., Kohnert,U., Rudolph,R., Fischer,S. and Martin,U.
Derivative of Lissue plasminogen activator
Patent: Ep 0400545-A 2 05-DEC-1990;
BOEHRIGER MANNERM CARBH
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                                                                                                                                                                                Synthetic DNA encoding new t-PA tissue plasminogen activator.
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                                 TGTACACAAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
                                                          1259 TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1311
                                                                                                                                                                                                                                                                                                                synthetic construct
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1 (bases 1 to 1314)
Niwa, M., Salto, Y., Sasaki, H., Hayashi, M., Notani, J. and
Kobayashi, M.
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larity 99.5%; Pred. No. 6.5e-244;
Conservative 0; Mismatches 5;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/product='t-PA'
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1 (Dases I to 1419)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and
Kobayashi,M.
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Pred. No. 6.5e-244;
0; Mismatches 5;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                      New tissue plasminogen activator
Patent: EP 0302456-A 49 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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94.4%; Score 1065; DB 6;
Best Local Similarity 99.5%; Pred. No. 6.5e-244;
Matches 1068; Conservative 0; Mismatches 75;
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/mol type="genomic DNA"
/db_xref="taxon:32630"
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596 884 656 944 716	QY         776 AGCTCTCCGGCTACGGCAAGCATGTCTCTTTCTATTCGGAGCGGTGAAGG 835           Db         1064 AGCTCTCCGGCTACGGCAAGCATGTCTCTTTCTATTCGAGCGGTGAAGG 1123           Db         1064 AGCTCTCCGGCTACGGCAAGCGTTGTCTCTTTACGGAGCGTGAAGG 1123           QY         836 AGGCTCATGTCAGATGTTCCATCCACCGCTGCACATTTACTTAACAGAA 895           Db         1124 AGGCTCATGTCAGACTTCACACCCATCCAGCCGCTGCACATTACTTAACAGAA 1183           QY         896 CAGTCACCGAACAACTGTGCTGGTGCTGGAGACACTCGGAGCGCCCCAGGCAAACT 955	Db   1184 CAGTCACCGACAACATGCTGTGTGTGTGTGTGTGTGGGGGGGG	RESULT 7 AR05996 LOCUS DEFINITION REQUERCE 62 from patent US 5840533. DEFINITION ROS9996 VERSION VERSION VERSION NECESSION NECESSION VERSION VERSION NECESSION NECESSI	Query Match         94.4%;         Score 1065;         DB 6;         Length 1419;           Best Local Similarity         99.5%;         Pred. No. 6.56-244;         Added         O;         Gaps         O;           Matches 1068;         Conservative         0;         Mismatches         5;         Indels         0;         Gaps         O;           Qy         5 CCCAGGCGCTCTCTGAGGGAAACAGTGCTTTTCGGAATGGGTCAGCTACCGTG         115         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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944 ATGACATTGCGCTGCTGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGCAGCG
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                                                          656 ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCG
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Multihill, B.R., Nexo, B.A., Yoshitake, S., Ikeda, Y., Suzuki, S.,
Hashimoto, A. and Yuzuriha, T.
Mutant t-PA with Kringle replacement
Patent: EP 0293934-A1 44 07-DEC-1988;
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Sequence 44 from Patent EP 0293934.
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1 (bases 1 to 1419)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and
Kobayashi,M.
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Pred. No. 6.5e-244;
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/mol_type="genomic DNA"
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/dol_xref="taxon:32630"
/dol_413 c 426 g 271 t
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Pred. No. 6.5e-244;
0; Mismatches 5;
                                      Yoshitake, S.,
                         1 (bases 1 to 1689)
Mulvihil, E.R., Nexo, B.A., Yoshitake,
Hashimoto, A. and Yuzuriha, T.
Mutant t.PA with kringle replacement
Patent: EP 0293934-A1 46 07-DEC-1988;
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                                                                                      Location/Qualifiers
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AGCTCTCCGGCTACGCCAAGCATGAGGCCTTGTCTTTCTATTCGGAGCGGCTGAAGG

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KTOMLYQQIQOSULRPULRSNRVEYCOKTOSGAQCHSVPVGSCBROCFNGGTCQQALY
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/protein id="CAA06577.1"
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Bollen,A.J., Gheysen,D., Jacobs,P., Pierard,L. and Collen,D.J.
Patent: WO 8804690-A 3 30-JUN-1988;
Location/Qualifiers
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/transl_table=11
/product="mutant tissue plasminogen activator (t-PA)"
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/protein_id="c1490688.1"
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SCARRDAILITGLGARINYCRUPDRDSEWCYVPTAGKSGSESECGSTPAGSGGNSDCYFG
NGAYRGTHSILTEGARINYCRUPDRDSENDEN TAGKYTAQURSAQALGLGKHNYCRNPDGDAKP
WCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRR
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IVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYG
KHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDA
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                                                                                                                                                                                                                                                                              1590 TGACTTTGGTGGGCATCATCAGCTGGGGCTGTGGACAGAAGGATGTCCGGGTG
                                                                                                       1530 TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCTGGTGTGTCTGAACGATGGCCGCA
                                                                                                                                                                                                                    1016 TGACTTTGGTGGGCATCATCAGCTGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTG
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TGCACGACGCCTGCCAGGCCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA
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synthetic construct
artificial sequences.

1 (bases 1 to 1780)
Petersen, L.C. and Boel, E.
A tissue plasminogen activator analogue
Patent: EP 0351246-A 7 1-JAN-1990,
NOVO-NORDISK A/S, NOVO NORDISK A/S
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Pred. No. 6.5e-244;
0; Mismatches 5;
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/organis="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/replace="agt"
misc_difference 1367. 1372
/note="in t-PA K419S, H42OT"
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/note="in t-PA CB7S, K419S"
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C12N9/52,A61K35/12,A61K35/74,A61K37/02,A61K37/54,C07H21/04, PC
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/product='this-kringle plasminogen activator'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product='this-kringle plasminogen activator'
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /product='signal peptide of urokinase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1836;
              synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 1836)
Pooru, P.H., Narendaa, K.K. and Shiyouguangu, R.R.
POLYCLINGIB PLASMINGEN ACTIVATING FACTOR
PATENT: JP 1987104577-A 1 15-MAY-1987;
AMERICAN HOME PROD CORP
OS Artificial gene
OC Artificial sequence; Genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                              13.AUG-1986 JP 1986191173
14.AUG-1985 US 85 766163, 11.-JUL-1986 US
POOUEN HANGU, NARENDAA KUMAARU KARUYAN, PI
                                                                                                                                                                                                                                                                                 (C12N9/52,C12R1:19), (C12N15/00,C12R1:19), strandedness: Double;
                                                                                                                                                                                                                                                                                                   strandcures..
topology: Linear;
hypothetical: No;
anti-sense: No;
*Source: cell type=fibroblast;
*source: cell_line=WI-38cell;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.4%; Score 1065; DB 6;
llarity 99.5%; Pred. No. 6.5e-244;
Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1836
/organism="synthetic construct"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/d_537 c 528 g 349 t
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                                                                                                                                                        homo sapiens
JP 1987104577-A/1
15-MAY-1987
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Best Local Similarity
Matches 1068; Conserv
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AUTHORS
TITLE
JOURNAL
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                            TAGGCAAGGTTTACACACACACACACCCCAGTCCCCAGGCACTGGGCCTGGGCAAACATA
                                            TAGGCAAGGTTTACACACACACACACACCCCAGTGCCCCAGGCACTGGGCCTGGGCCAAACATA
                                                                                                                                         GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA
                                                                                                                                                              GCTGACGTGGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA
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S Hung, P. P., Kalyan, N.K. and Lee, S.-g.L.

Poly-kringle plasminogen activator

AL Patent: US 4916071-A 1 10-APR-1990;

American Home Products Corporation; New Yor

Location/Qualifiers

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/\*tag= a //\*tag= hompA-K2S fusion protein" /product= "OmpA-K2S fusion protein" /transl except= (pos:1126..1128, aa:Pro-Gly) /note= "No stop codon"

'partial

Location/Qualifiers 1..1128

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Glycosylated plasm
Sequence encoding
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Tissue type plasmi
Musated t-PA analo
Part of tPA024 gen
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                                                                                                         Entire sequence of
Plasmid pEMp1-tPA.
Novel plasminogen
Novel plasminogen
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Sequence of coding
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Plasmid pKG12 cont
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AAQ05534
AAQ12072
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AAN91120
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87GB-0025052.
87GB-0026683.
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26-OCT-1987;
13-NOV-1987;
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03-OCT-2002
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                                                                                                                                                                                                                                                                                                          secreted, active contracts to a method the plasminogen activator (FPA), Kringle 2 serine protease molecule (K2S) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants. Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain, peripherally occluded arteries, coronary artery occlusion, deep vein thrombosis or related diseases associated with unwanted blood clotting. The present sequence is a DNA encoding a fusion protein comprising OmpA and K2S protein.
                                                                                                                                                                                 activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
                                                                                                                                                                                                                                                                                                invention relates to a method of producing extracellularly
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                                                                                                                                                                  Producing active, correctly folded recombinant tissue plasminogen
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                                                                          Manosroi J,
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100.0%; Pred. No. 5.1e-239;
ive 0; Mismatches 0;
                                    (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                                        Tayapiwatana C,
                                                                                                                                                                                                                                                        Claim 7; Page 30; 80pp; English
14-NOV-2000; 2000GB-0027779
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                                                                                                         WPI; 2002-519376/55.
P-PSDB; AAE25034.
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Best Local Similarity
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1019 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTAACTAAACAGAA 1078
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                                                                                                                      1139 TGCACGACGCCTGCCAGGCGATTCGGGAGCCCCCTGGTGTGTCTGAACGATGGCCGCA
                                                                                                                                                               1016 TGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAAGGATGTCCCGGGTG
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                                                                                                                                                                                                                      This sequence encodes a non-glycosylated tPA deriv. lacking the finger- and EGF-domains. The polypeptide has a lower clearance rate (longer half-life) than natural tPA while retaining thrombolytic activity and stimulation by fibrin. (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New non-glycosylated form of tissue plasminogen activator - with thrombolytic activity and long plasma life
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Pred. No. 3.9e-225;
0; Mismatches 5;
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/product=tPA deriv.
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Best Local Similarity 99.5%;
Matches 1068; Conservative
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 Hayashi M, Notani J,
                                                                                                                                                            (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
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Best Local Similarity 99.5%; Pred. No. 3.9e-225;
Matches 1068; Conservative 0; Mismatches 5;
                                                                                                                                 Disclosure; Page ?; 68pp; English.
Sasaki H,
                           WPI; 1989-040625/06.
P-PSDB; AAP94409.
Saito Y,
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                                                                                                                                     Tissue plasminogen activator; tPA; thrombolytic agent; plasminogen; vascular diseases.
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99.5%; Pred. No. 3.9e-225;
tive 0; Mismatches 5;
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            BP.
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87GB-0025052.
87GB-0026683.
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            DNA;
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P-PSDB; AAP94416.
            standard;
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Matches 1068; Conserv
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26-OCT-1987;
13-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                One N-glycosylation site, i.e. NSS (117-119) is substituted with NSM and the N-glycosylation is removed.

Plasmid encoding the modified tPA is 99-6300 and its transformant is E.coli RR1-Zem 99-6300 (FERM P-9127).

This modified tPA, used to treat thrombosis, is of high quality and has a longer half life period in blood.

See also AAN82177-N82179.

(Updated on 10-MAR-2003 to add missing OS field.)

(Updated on 25-WAR-2003 to correct PF field.)

(Updated on 25-WAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1065; DB 9; Length 1689;
Pred. No. 4e-225;
0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                   Modified tissue plasminogen activator - having glycine-183 residues sustd. With serine and threonine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1689 BP; 376 A; 482 C; 504 G; 327 T; 0 other;
/product=modified tPA
                                                                                                                                                                                                                                                                                                      Disclosure; Page ?; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%;
                                                                                                                                  87JP-0064339
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Best Local Similarity 99.5'
Matches 1068; Conservative
                                                                                                                                                                  COLLID
                                                                                                                                                                                                 WPI; 1988-311961/44.
P-PSDB; AAP82581.
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                              AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGACACTTACGACA
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Pred. No. 4e-225;
0; Mismatches 5; Indels 0;
                                                            New tissue plasminogen activator (t-PA) analogue -
with higher fibrin selectivity than native t-pa, useful for
treating infarction, thrombosis and embolism
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1780 BP; 405 A; 513 C; 523 G; 339 T; 0 other;
                                                                                                                             Disclosure; Fig 5A-D; 24pp; English
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Best Local Similarity 99.5%;
Matches 1068; Conservative
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                                                                                                                                 Gарв
                           and
                       cDNA sequence of native tPA gene is excised from plasmid pST112, digested with Banmil and Sal1 to form plasmid pST118. (Updated on 03-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                         2100;
                                                                                                          Length
                                                                                                                                 Indels
                                                                                 Sequence 2100 BP; 498 A; 595 C; 597 G; 410 T; 0 other;
                                                                                                         Query Match 94.4%; Score 1065; DB 10; Best Local Similarity 99.5%; Pred. No. 4.1e-225; Matches 1068; Conservative 0; Mismatches 5;
   Example 29; Fig 21; 68pp; English
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                                                                     AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTTTCTATTCGGAGCGGCTGAAGG
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                                                                                                                                                                                                                                                                                                                         Kobayashi M;
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P-PSDB; AAP94406.
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26-OCT-1987;
13-NOV-1987;
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03-OCT-2002
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 GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
                                                      TAGGCAAGGTTTACACACACACACAGTGCCCAGGCACTGGGCCTGGGCAAACATA
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                                                                                                                         TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tissue plasminogen activator - having N-terminal peptide of plasminogen linked to tissue plasminogen activator for increased stability in vivo.
                                                                                                                                                                                                                                                                                                    Plasmid pST112 encoding novel N-terminal for tissue plasminogen activator (tPA).
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llarity 99.5%; Pred. No. 4.1e-225;
Conservative 0; Mismatches 5; Indels 0;
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                                                                                                         Intron, recombination, combinatorial gene; trans-splicing;
gene therapy, polymerase chain reaction, PCR; primer; amplification;
tissue plasminogen activator; tPA; plasmid TPA-KS+; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A cDNA clone of human tissue plasminogen activator (tPA) was amplified by PCR using the primers given in AAQ87368-69. The amplified tPA DNA (AAQ8730) was ligated into vector KS+ to obtain plasmid TPA-KS+. The construct was used in combinatorial methods involving RNA splicing-mediated shuffling of tPA domains implasmid pINVI (AAQ87347) to generate novel tPAs having improved thrombolytic properties.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New intron-mediated recombinant techniques - used for the generation and selection of novel genes and gene prods. for use in therapy
                                                                                                                                                                                                                                                           *tag= a
note= "signal sequence and finger-like domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1065; DB 16;
Pred. No. 4.1e-225;
0; Mismatches 5;
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/product= Kringle-1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                      'product= EGF-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 59-60; 87pp; English.
                                                                                                                                                                                                                          Location/Qualifiers
82..334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.5%;
Matches 1068; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US10146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0119512.
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/product= 1
973..2162
/*tag= e
                               (updated)
(first entry)
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                                                                                                                                                                                                                                                                                        335..447
/*tag= b
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                                                                             Human tPA clone.
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sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9507351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-1993;
                            25-MAR-2003
19-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jarrell KA;
                                                                                                                                                                                          Synthetic
AAQ87370;
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GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCT

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GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA

ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCA 875 ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCA GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACACAGTACA

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GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC

416 AGGCTGCCATCTTTGCCAAGCACAAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGCA 1055 AGGCTGCCATCTTTGCCAAGCACAGGAGGTCGCCGGAGAGGGGTTCCTGTGCGGGGCA 476 TACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGGTTTCCGC

GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGC

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TACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGGAGGTTCCGC

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CCCACCACCTGACGTGATCTTGGGCAGAACATACCGGGTGGTCCTTGGCGGGAGGAGGAGC

AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA

CCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC

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The present sequence represents the human tissue plasminogen activator gene. It was used to construct plansid TPA-KB+, which is used in the course of the invention. The specification describes a purified creverse-splicing introm which comprises a segment comprising a 5 rpart of a group II introm, including an exon binding site not 3 rpart of a group II introm, including a domain V motif, a branch site acceptor, and a nucleophilic group for transesterifying a phosphodiester bond of an RNA. Together the two segments form an contractalytic Y-branched introm which catalyses integration of at least the reverse-splicing introms which catalyses integration of at least the reverse-splicing introms are used, by specific cleavage and ligation of discontinuous nucleic acid, to generate new genes and gene products, c.g. ribozymes (for use in gene therapy or as reagents in DNA manipulation, e.g. replacements for restriction enzymes) or immunologically active or signal-transducing proteins such as antibody immunologically active or signal-transducing proteins such as antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reverse splicing construct containing fragments of autocatalytic introns - able to cleave and ligate discontinuous nucleic acid for generating new genes and e.g. ribozymes, libraries of enzymes and antibodies
                                                                                                                                                                                                           finger-like domain"
                                             Plasmid pINVI; reverse-splicing intron; group II intron;
exon binding site; domain V motif; branch site acceptor;
nucleophilic group; transesterification; phosphodiester bond;
autocatalytic Y-branched intron; reverse splicing reaction; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2162 BP; 520 A; 606 C; 619 G; 417 T; 0 other;
               tissue plasminogen activator gene sequence
                                                                                                                                                                                            *tag= a
note= "signal sequence and
                                                                                                                                                                                                                                                                                                                                                                                       '*tag= e
'note= "catalytic domain"
                                                                                                                                                                                                                                                                                                                                      *tag= d
note= "Kringle-2 domain"
                                                                                                                                                                                                                                                                                         *tag= c
note= "Kringle-1 domain
                                                                                                                                                                                                                                         '*tag= b
'note= "EGF-like domain'
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                                                                                                                                                           Location/Qualifiers
82..334
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                                                                                                                                                           Key
misc_feature
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                                                                                                      ATGACATTGCGCTGCTGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCG
                                                                                                                                                                                                                                                                                                TGGTCCGCACTGTGTGCCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTG
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Matches 1068; Conservative

Local Similarity

Query Match

Length 2162; Indels

Score 1065; DB 19; Pred. No. 4.1e-225;

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1240 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA 1299
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                                                                 GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC
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                                                  GCCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTGCCGGCCTGAGACAGTACA
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                                                                                                                                                                  416 AGGCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCA
                                                                                                                                                                                                                           TACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGC
                                                                                                                                                                                                                                                                                     CCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patentors claim a novel recombinant human t-PA which is resistant to specific enzymatic cleavage because it is stabilised by site-directed mutagenesis at a 2-chain cleavage site. Partic. the natural Arg at position 275 is replaced by Gly or Glu, or 11e at position 276 is replaced 75 is replaced by Gly or Glu, or 11e at position 276 is replaced (275 and 276 refer to the posn. of the AAB in the mature protein; i.e. AAB 310 and 311 of AAP60790). Also new are (1) DNA sequences; (2) expression vectors; and (3) microorganisms and cell cultures transformed with these vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGGCGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG
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.larity 99.5%; Pred. No. 4.2e-225;
Conservative 0; Mismatches 5; Indels 0
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                                                                                                                     Sequence encoding human pre-tissue plasminogen
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P-PSDB; AAP60790.
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Best Local Similarity
Matches 1068; Conserv
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01-APR-1986;
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/note= "from immunoglobulin kappa light chain gene"
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/label= TPA cDNA
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(Updated on 25-MAR-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 94.4%; Score 1065; DB 10; Best Local Similarity 99.5%; Pred. No. 4.2e-225; Matches 1068; Conservative 0; Mismatches 5;
                                                 ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            14-JUN-1988;
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Homo sapiens
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Vector pEMp1-tpa is an example of a vector of the invention. Pref. the blocking element is a promoter sequence oriented with its native disposed proximal to the enhancer element and its 5' end disposed distal to the enhancer element. Alternatively the interposed blocking element comprises a promoter sequence with its 5' end disposed broximal to the enhancer element and, at its 3' end, a gene encoding for a different protein of interest, (see FT). The vector pEMp1 was constructed by inserting an enhancer-blocking element into pEM1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPA CDNA fragment was inserted into the unique XhoI site present in both pEM1 and pEM1. Of 26 transformants obtd. with pEM1-tpa, 5 produced TPA at levels of 140-500 IU/ml. Of 16 transformants obtd. with pEMp1-tpa, 7 produced TPA at levels of 1000-6000 IU/ml. (Updated on 31-0CT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                         chain (IgH)"
                        /note= "contg. the ampicillinase gene and the bacterial origin of replication"
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note= "from immunoglobulin heavy
                                                                                                                                                                                                                                    /note= "functions as a blocking 6972..7281
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blocking element so that marker protein is
levels required for selection
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/label= SV40 origin region
                                                                       .coli gpt gene
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/label= SV40 (gpt) CAP
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|abel= lambda-1
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(ABBO ) ABBOTT
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Score 1065; DB 8; Length 7533; Pred. No. 4.8e-225;

94.4%; 99.5%;

Query Match Best Local Similarity

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                                                                                                         GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
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                                                                                       GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
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                               CCCAGGCGGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG
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note="f<u>r</u>om Ig kappa light chain gene"
930..1935
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note="kappa 3 flanking sequence'
105..4463
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'note="from metallothioneine I"
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/note="from lambda promoter"
5946..6971
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label=pSV2-gpt
note="non-coding strand"
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/trag= i
/label=origin_region
/note="from SV40"
6548..6619
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label=Cap_site
note="from_SV40(gpt)
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'note="lambda mRNA"
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note="from SV40"
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note="from IgH"
282..7466
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533..6650
                       AAN81970 standard; DNA; 7533 BP.
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label=tPA_cDNA
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/label=pBR322
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.956..2104
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                                                                     (first entry)
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                                                                                            Plasmid pEMp1-tPA
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                                                                                                                                                       Homo sapiens
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                                                                     12-OCT-1990
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                                                                                                                                                                                                                                                               3'UTR
RESULT 14
AAN81970
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The plasmid was prepd by cleaving the very long 3' UT of t-Ph cDNA (which causes mRNA instability) 34 nucleotides downstream of stop codon and inserting it into a pEMp1 vector. The pEMp1 vector was constructed from the following components (see feature table):

(a) a 2.25 PvuII-BamHI fragment from pSV2-gpt contg. the SV40 enhancer and early region promoter, the E.coli gpt gene, the SV40 small tumour antigen intervening sequence, and the SV40 termination and polyadenylation signals;

(b) a 2.3 kb PvuII-BcoRI fragment from pBR32 contg. the ampicillinase gene and the bacterial origin of replication;

(c) a 0.3 kb PvuII-BcoRI fragment contg. an Ig heavy chain enhancer;

(d) a 0.2 kb SacI-BgIII fragment contg. the metallothioneine I romoter;

(e) a 0.4 kb AvaII-HaeIII fragment contg. the 1g light chain promoter,

(f) a 0.26 kb xbal-bscNI fragment contg. the Ig light chain promoter,

TATAA sequence, and the initiation site.

The expression plasmid can be used to transform host cells esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              933 GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    873 GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           633 ccccreccrecreaedeaaacagreacrecracrireegaaregercaeccracere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 GCACGCACAGCCTCACCGAGTCCGCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 TAGGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodn. of human tissue plasminogen activator - by myeloma cells, pref. in presence of epsilon amino caproic acid.
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94.4%; Score 1065; DB 9; Length 7
Best Local Similarity 99.5%; Pred. No. 4.8e-225;
Matches 1068; Conservative 0; Mismatches 5; Indels
                                                                    /label=cap_site
/note="from metallothioneine I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page ?; p; English.
                                                                                                                                                                                                                                                                                                                              87WO-US01569.
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7467..7533
                                         tag= q
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P-PSDB; AAP81913.
protein bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCA 965
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                                                                                                                                                                                                                                                                                                                                                                            A DNA construct (AAT27586) codes for a novel plasminogen activator (AAR96222) in which the kringle KI domain (AAR96221) of plasminogen replaces the native KI domain of tissue plasminogen activator (tPA) (AAR96220). It was obtd. by inserting a synthetic plasminogen KI domain DNA (AAT27586) into tPA DNA and can be expressed in transforated Becherichia coli RRI cells (FEMA P9272). Novel plasminogen activators are produced that show increased clot lysing specificity or plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                               Hybrid plasminogen activator comprises human tPA activator and N-terminal crosslinking domain from alpha2-plasmin inhibitor useful to treat thrombosis and image blood clots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
94.3%; Score 1064; DB 17; Length 1680;
Best Local Similarity 99.5%; Pred. No. 6.6e-225;
Matches 1067; Conservative 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1680 BP; 387 A; 471 C; 479 G; 343 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 11; 35pp; English.
                                                                                                                92US-0827587.
                                                               94US-0254485
                                                                                              87US-0125629
                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                              WPI; 1996-187699/19.
P-PSDB; AAR96223.
                                                                                             25-NOV-1987;
28-JAN-1992;
06-JUN-1994;
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USS504001-A
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                                                                                                                                           CCCACCACCTGACGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; tPA; alpha2-plasmin inhibitor; fibrinolytic; thrombolytic; fibrin; thrombosis; blood clotting; protein engineering; kringle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/*tag= a
106..1677
/*tag= b
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06-AUG-1996
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Search completed: August 18, 2003, 23:28:52 Job time : 398.386 secs

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US-08-811-949-58 US-08-417-640-3 US-08-411-949-60 5185259-2 US-08-451-640-7 US-08-558-269-5 US-09-410-882-5 5244676-4 US-08-811-949-40 5200340-3 US-09-643-597-122 US-09-643-643-122 US-09-643-642-122 US-09-606-421B-122

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ALIGNMENTS

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Sequence 62, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 3, Appli
Sequence 25, Appli
Sequence 48, Appl
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Listing first 45 summaries
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Sequence 39, Appl Sequence 1, Appli Sequence 1, Appli Sequence 44, Appl Sequence 50, Appl Sequence 63, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl

US-08-286-740-1 US-08-286-740-1 US-08-811-949-44---US-08-811-949-50 US-08-811-949-64 US-08-811-949-64 US-08-811-949-64 US-08-811-949-54 US-08-811-949-54 US-08-811-949-54 US-08-811-949-54 US-08-811-949-54

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Sequence Seq

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Patent No. 52 Sequence 5,

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                                                                                          Sequence 10, Application US/08814412

Patent No. 6150141

GENERAL INFORMATION:

APPLICANT: Jarrell Ph.D., Kevin A.

TITLE OF INVENTION: Intron-Mediated Techniques and Reagents
NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
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Pred. No. 8.6e-290;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Vex CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,412
FILING DATE: 11-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jarrell Ph.D., Brenda H.
REGISTRATION NUMBER: 33,223
REFERENCE/DOCKET NUMBER: 0079571-004
TELECHONE: 617 248 5000
TELEFRAX: 617 248 4000
                                                                                                                                                                                                                           E: Choate, Hall & Stewart
53 State Street
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 99.5
Matches 1068; Conservative
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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CITY: BO
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Pred. No. 7.7e-290;
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ADDRESSEE: P.C.
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HORASHI, MASAKO
APPLICANT: HORASHI, MASAKO
APPLICANT: TOBAYASHI, MASAKO
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APPLICANT: TOBAYASHI, MASAKO
APPLICANT: TOBAYASHI, MASAKO
APPLICANT: ADBAYASHI, MASAKAZU
APPLICANT: OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
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Patent No. 5840533
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ZIP: 22202
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 18-966-0
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELEFRAX: 703-413-3000
TELEFRAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOBLICATION CONTRACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1065; DB 2;
Pred. No. 9.1e-290;
0; Mismatches 5;
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995 GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC 1054
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                                                                                                     NAWE/KEY: misc_feature
LOCATION: 448..714
OTHER: INFORMATION: /product= "Kringle-1 domain"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 715..972
OTHER INFORMATION: /product= "Kringle-2 domain"
                                                                                                                                                                                                                                                                .; NAME/KEY: misc_feature
; LOCATION: 973..2162
; OTHER INFORMATION: /product= "Catalytic domain"
US-08-119-512-3
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 94.4%; Score 1065; DB 1;
Best Local Similarity 99.5%; Pred. No. 9.2e-290;
Matches 1068; Conservative 0; Mismatches 5;
                    NAME/KEY: misc_feature
LCCATION: 335..447
OTHER INFORMATION: /product= "EGF-like |
FEATURE:
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                    1358 AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCTCTTTCTATTCGGAGCGGCTGAAGG
TGGTCCGCACTGTGTCCCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTG
                                                                                     AGCTCTCCGGGCTACGGCAAGCATGAGGCCTTGTCTCTTTCTATTCGGAGCGGCTGAAGG
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Patent No. 5498531
CENERAL INFONTION:
TITLE OF INVENTION:
INTRON MEDIATED RECOMBINANT TECHNIQUES
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY:
STREET: MA
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LOCATION: 82..334
OTHER INFORMATION: /product= "Signal Sequence and
OTHER INFORMATION: Finger-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIPHIATOR COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP PC compatible
COMPUTER: EMP PC compatible
COMPUTER: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,512
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPRENCE/DOCKET VINDRER: HUI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-119-512-3
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415

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1415 AGCTCTCCGGCTACGGCAAGCATGAGCCTTGTCTCTTTCTATTCGGAGCGGCTGAAGG 1474
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                                                                                                                                                                                                                                                                                                                                                  56 CCCAGGCGGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG
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                                                                                                                                                                                                                                                        Length 2162;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                              "Kringle-2 domain"
/product= "Kringle-1 domain"
                                                                                                                                     Score 1065; DB 1;
Pred. No. 9.2e-290;
0; Mismatches 5;
                                                                    LOCATION: 715. 972
OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                          94.4%;
                                              misc_feature
715..972
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.55
Matches 1068; Conservative
  OTHER INFORMATION:
                        FEATURE:
NAME/KEY:
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                                         TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA
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                                                                                                                                               CAGTCACCGACAACATGCTGTGTGCTGCAGACACTCCGAGGCGGCGGCCCCCAGGCAAACT
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APPLICANT: Jarcell, Kevin A.

TITLE OF INVENTION: AND REAGENTS

TUTLE OF INVENTION: AND REAGENTS

CORRESPONDENCE ADDRESS:

ADDRESSES: Foley, Hosq & Bliot

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 82..334
OTHER INFORMATION: /product= "Signal Sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 335..447
OTHER INFORMATION: /product= "EGF-like domain"
FRATURE:
NAME/KEY: misc_feature
LOCATION: 448..714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109
COMPUTER RADABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,015B
FILING DATE: US/08/ASPOTION OF UNA-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPERENCE/DOCKET NUMBER: HUV-008.02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STATEMENT (617) 832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACTERISTICS:
LENGTH: 2162 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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OTHER INFORMATION: Finger-like domain"
FEATURE:
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Patent No. 5780272
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1175 CCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC 1234
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  875 ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCA 934
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Fatent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
WUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
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                                                                                            TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/08488015B
Fatent No. 5780272
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STREET: One Post Office Square
CITY: Boston
STREET: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,015B
FILING DATE: O'-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REGISTRATION INFORMATION:
TELEPHONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
TURNEY, APPLICATION DOC 25:
SEQUENCE CHARACTERISTICS:
TURNEY, AND DOC 25:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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US-08-488-015B-25
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   719 CCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC 778
                                                              779 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA
                                                                                                                                                                                                                                                              776 AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTTCTTCTATTCGGAGCGGCTGAAGG
                                                                                                                                    839 ATGACATTGCCCTGCAGCTGAATCGGATTCGTCCCCCTGTGCCCAGGAGAGCAGCG
                                                                                                                                                                                          TGGTCCGCACTGTGTCCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGAGTGTG
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                                                                                                                656 ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCCAGGAGAGCAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *, APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA, ; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI ; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 2.4e-289;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.3%;
Best Local Similarity 99.4%;
Matches 1067; Conservative
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94.3%; Score 1063.4; DB 2; Length 1314;
Best Local Similarity 99.4%; Pred, No. 2.1e-289;
Matches 1067; Conservative 0; Mismatches 6; Indels 0;
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: 'VA COUNTRY: USA
                                                                                                                                      COMPUTER REALABLE CURVII.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELEPHONE: 703-413-2200
TELEPHONE: 703-413-2220
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                        ZIP: Z2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION:
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Query Match
Best Local Similarity 99.4%;
Matches 1067; Conservative
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-883-795A-39
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  GCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA
               GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC
                                                                   GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCCACCCTGGC
                                                                                                        AGGCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGCGTTCCTGTGCGGGGGCA
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Tissue Plasminogen Activator
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US-08-883-795A-39
US-08-883-795A-39
Sequence 39, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Delcuve, Genevieve
TITLE OF INVENTION: Recombinant DNA;
TITLE OF INVENTION: Vectors for Tiss
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: BERESKIN & PARR
STREET: 40 King Street West
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COMPUTER READABLE FURN:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF S64-7311
TELECOMMUNICATION OF S64-7311
TELECOMMUNICATION OF S65
SEQUENCE CHARACTERISTICS:
TEMPORMATION FOR S60 ID NO: 39:
SEQUENCE CHARACTERISTICS:
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Pred. No. 2.5e-289;
0; Mismatches 6;
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 CAGTCACCGACAACATGCTGTGTGTGCTGGAGACACTCGGAGCGGCCGCGGCCCCAGGCAAACT
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; Patent No. 5561053
; GENERAL INFORMATION:
    TITLE OF INVENTION: METHOD FOR SEL
    TITLE OF INVENTION: HOST CELLS
    TITLE OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 460 Point San Bruno Blvd
    CITY: South San Francisco
    STATE: California
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ZIP: 94080
COMPUTER READABLE FORM:
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1424 AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGG
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                    1304 ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGAGCAGCG
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LEMONYT, JEFFREY F.; DACKOWSKI, WILLIAM; DOUGLAS, RICHARD;
COLE, EDWARD S.; PURCELL JR., RICHARD D.;LAU, DAVID TAI-YUI
JITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN
JACTIVATOR PRODUCED BY RECOMBIANT DNA
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
JAPPLICATION NUMBER: US/07/782,686
FILING DATE: 01-OCT-1985
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRING DATE: 01-OCT-1984
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94.3%; Score 1063.4; DB 6

Best Local Similarity 99.4%; Pred. No. 2.7e-289;

Matches 1067; Conservative 0; Mismatches 6;
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Best Local S
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3135 TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTTCTGAACGATGGCCGCA 3194
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2835 ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGG
                                                                                                                                                                                                                                                                                                                                                 3015 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAA 3074
                                                                                                                                                                                                          2955 AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3195 TGACTTTGGTGGGCATCATCACAGCTGGGGCCTGGGCTGTGGACGACGAAGGATGTCCCGGGTG
                                                                                                2895 IGGICCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        956 TGCACGACGCCTGCCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1016 TGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTG
                                                                716 TGGTCCGCACTGTGTCCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTG
                                                                                                                                                                             776 AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTTCTTTTCGGAGCGCGCTGAAGG
                                                                                                                                                                                                                                                                                            836 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                        896 CAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGGGCCCCCAGGCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076 TGTACACAAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
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Sequence 1, Application PC/TUS9509576

APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
TITLE OF INVENTION: MOST CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: 4
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZUMANTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patrin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/09576 FILING DATE: CLASSIFICATION DATA: PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATE: CLASSIFICATION DATE: CLASSIFICATION DATE: 08/286740 FILING DATE: 05-AUG-1994 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 791
TELECOMMUNICATION INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7360 heart
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY:
PCT-US95-09576-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2475 GGCTGACGTGGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGGCCTGAGACAGTACA 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2355 TAGGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA 2414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2715 cccaccaccreacegrearcrregecagaacaracegeregrecregeceaesassec 2774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2775 AGAAATTTGAAGTCGAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA 2834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2295 GCACGCACAGCCTCACCGAGTCGGTGCCTCCTGCCTCCGTGGAATTCCATGATCCTGA 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,740
FILING DATE: US-AUG-1994
CLASSIFICATION 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: DE-MEMORY M.
BACTORNEY/AGENT INFORMATION:
BACTORNEY/AGENT INFORMATION:
BACTORNEY/AGENT MARGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1063.4; DB 1
Pred. No. 4.3e-289;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 7360 bases
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Best Local Similarity 99.4%;
Matches 1067; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-286-740-1
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AATCCTGATGGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 TACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCCAAACATAATTACTGCCGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGG
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1076 TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
                      3255 TGTACACCAAGGTTACCAACTACCTAGATTCGTGACAACATGCGGCG
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                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTKI: ____
ZITE: _____
ZITE: _____
ZITE: _____
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MA-1997
CLASSIFTATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                  Sequence 44, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYSHI, HITOSHI
APPLICANT: NOTANII, JOUJI
APPLICANT: NOTANII, JOUJI
I TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.1%; Score 1062; DB 2; )
Best Local Similarity 100.0%; Pred. No. 4.8e-289;
Matches 1062; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1068 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circular
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; LOCATION:
US-08-811-949-44
                                                                                        RESULT 13
US-08-811-949-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                              JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEFAK: 703-413-3000
TELEFAK: 703-413-3220
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Pred. No. 6e-289;
0; Mismatches 7;
                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 99.3%;
Matches 1066; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ADDRESSEE: P.C.
STREET: 1755 S.
CITY: ARLINGTON
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US-08-811-949-50
                                                                                     STATE: VI
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US-08-811-949-50
Sequence 50, Application US/08811949
Settl-949-50
Sequence 50, Application US/08811949
Settl-0540533
GENERAL INFORMATION:
APPLICANT: NAITO, YOSHIMASA
APPLICANT: SAJAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                         Score 1061.8; DB 2;
Pred. No. 7e-289;
0; Mismatches 7;
TELEPHONE: 703-413-3000
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1974 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
NOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                         94.1%;
llarity 99.3%;
Conservative 0
                                                                                                                                                                                          ) NAME/KEY: CDS
; LOCATION: 3..1583
US-08-811-949-38
                                                                                                                                                                                                                                                                                              Similarity
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Best Local Simi
Matches 1066;
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ADDRESSEE: OBLON, SPIVAK, MCLUBLILL...

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
MAPE: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
FRETERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-08-011-949-38
US-08-011-949-38
Sequence 38, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SALTO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: ROBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUB PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1079
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896 CAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACT 955	956 TGCACGACGCCTGCCAGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCA 1015	1411 HELACCALGECTISCLAGGSCGATTCGGGAGGCCCCCTGGTGTGTGTGTGGAGGATGGCCGGA 14/0 1016 TGACTTTGGTGGGGGTTCATCAGCTGGGGGCCTGGGGATGGAAGGATGTCCCGGGTG 1075	1471 TGACTTTGGTGGGCATCATCAGCTGGGCCTGGGCTGTGGAAGGATGTCCCCGGGTG 1530	1076 TGTACACAAAAGGTTACCAACTACATAGAATTCGTGACAACATGCGACG 1128	TGTACACAAAGGTTACCAACTACGTACTGGATTCGTGACACATGCGACG 1583	
896	926	1016	1471	1076	1531	
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Search completed: August Job time : 89.2804 secs

Sequence 159, App Sequence 46, Appl Sequence 15, Appl Sequence 123, Appl Sequence 124, Appl Sequence 160, Appl Sequence 160, Appl Sequence 160, Appl Sequence 161, Appl Sequence 164, Appl Sequence 1652, Appl Sequence 16438, Appl Sequence 16438, Appl Sequence 16438, Appl Sequence 1612, Appl Sequence 16438, Appl Sequence 237, Appl

Sequence 12715, Sequence 35, Appl

Perfect score:

Sequence:

OM nucleic

Run on:

Minimum DB Maximum DB

Database

Searched:

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APPLICANT: Aranya Manosroi
APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Taderiah Goetz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production
TITLE OF INVENTION: MAn-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.219001
CURRENT FILING DATE: 20001
PRIOR RAPLICATION NUMBER: 60/268,574
PRIOR PRILING DATE: 2001-01-14
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH. 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: coding OTHER INFORMATION: sequence for OmpA-K2S fusion protein
2 US-10-101-510-159
2 US-10-101-510-458
3 US-10-101-510-458
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US-10-033-528-237
US-09-918-995-12715
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
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       Sequence 6, Appli
Sequence 7, Appli
Sequence 4, Appli
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Sequence 144, Appli
Sequence 144, Appli
Sequence 15, Appli
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Sequence 5, Appli
                                                                                                                      August 19, 2003, 04:46:44; Search time 318.307 Seconds (without alignments) 7930.701 Million cell updates/sec
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                                                                                                                                                                                                                             1 atgaaaaagacagctatcgc.....ttcgtgacaacatgcgaccg 1128
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1: /cgn2 6/ptodate/2/pubpna/PCT_NEW_PUBCOMB.seq:*
2: /cgn2_6/ptodate/2/pubpna/PCT_NEW_PUB.seq:*
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                     GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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1. US-09-987-455-5

1. US-09-969-271-6

4. US-10-133-656-7

1. US-09-969-271-5

1. US-09-969-271-5

1. US-09-974-55-4

1. US-09-974-298-144

2. US-10-007-926A-433

4. US-09-880-503-15

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1. US-09-74-298-846-12748

1. US-09-735-705-122
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Maximum Match 100%
Listing first 45 summaries
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61 GCGGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACG 120

1 ATGADADAGACAGCATTGCAGTGCCACTGGCTGGTTTCGCTACCGTGGCCCAG 60

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Sequence 122, App Sequence 122, App Sequence 122, App Sequence 122, App Sequence 122, App

US-09-850-716A-122 US-09-897-778-122 US-09-466-396A-122 US-1117-982-122

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      Sequence 5, Application US/09987455
; Sequence 5, Application US/09987455
; Publication No. US20030049729A1
; GENERAL INFORMATION:
; APPLICANT: Aranya Manosroi
; APPLICANT: Chatchai Tayapiwatana
; APPLICANT: Chatchai Tayapiwatana
; APPLICANT: Chatchai Tayapiwatana
; APPLICANT: Rolf-Guenther Werner
; TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
; TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
; TITLE OF INVENTION: Methods for Large Scale Production
; TITLE OF INVENTION: Methods for Large
; TITLE OF INVENTION: MADER: 60/268,574
; FILE REFERENCE: 6652.1290001
; CURRENT FILING DATE: 2001-11-14
; RIOR APPLICATION NUMBER: G8 0027779.8
; RIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AAGGTTTACACAGCACAGAACCCCCAGTGCCCACTGGGCCTGGGCAAACATAATTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: sequence for OmpA-K2S fusion protein
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ORGANISM: Artificial Sequence
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Publication No. US20030096733A1
GENERAL INFORMATION:
APPLICANT: HOLMDAHL, Rikard
APPLICANT: LI, Jinan
TITLE REFERENCE: 3810/10577-US3
FILLE REFERENCE: 3810/10577-US3
CURRENT APPLICATION NUMBER: US/10/193,656
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US-09-969-271-6
; Sequence 6, Application US/09969271
; Patent No. US20020098179A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));
; TITLE OF INVENTION: Pharmaceutical Combinations
; FILE REFERENCE: PCS10951APME
; CURRENT PILING NUMBER: US/09/969,271
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 0025473.0
; RIOR APPLICATION NUMBER: GB 0025473.0
; RIOR SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0;
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US-09-969-271-6
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; Ratent No. US20020098179A1
; Fatent No. US20020098179A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));
; APPLICANT: Pfizer Limited (GB and EP (GB) only)
; TITLE OF INVENTION: Pharmaceutical Combinations
; FILE REPERENCE: PCS10951APME
; CURRENT APPLICATION NUMBER: US/09/969,271
; CURRENT FILING DATE: 2001-10-17
; RIOR APPLICATION NUMBER: GB 0025473.0
; RIOR APPLICATION NUMBER: GB 0025473.0
; RUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5.
                                                                                                                                                                                                            1567 TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA
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                                                      836 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAA
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Pred. No. 0;
0; Mismatches
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DATABASE ACCESSION NUMBER: Genbank / X07393
DATABASE ENTRY DATE: 1995-03-27
RELEVANT RESIDUES: (1)..(2509)
            PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/304,490
PRIOR APPLICATION NUMBER: US 60/305,182
PRIOR PLING DATE: 2001-07-10
PRIOR PRICK DATE: 2001-07-13
PRIOR PRICK DATE: 2010-07-13
NUMBER OF SEQ ID NOS: 18
SEQ ID NO
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Best Local Similarity 99.4%;
Matches 1067; Conservative (
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                                   TACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGC
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Molecules
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| Publication No. US20030049729A1
| GENERAL INFORMATION:
| APPLICANT: Aranya Manosroi
| APPLICANT: Jiradej Manosroi
| APPLICANT: Chacthai Tayapiwatana
| APPLICANT: Roif-Guenther Wenner
| TITLE OF INVENTION: DNA-Derived tPR or K2S Mole
| FILE REFERENCE: 0652.219001
| CURRENT APPLICATION NUMBER: 06/268,574
| PRIOR APPLICATION NUMBER: 60/268,574
| PRIOR FILING DATE: 2001-11-14
| PRIOR FILING DATE: 2000-11-14
| PRIOR FILING DATE: 2000-11-14
| PRIOR FILING DATE: 2000-11-14
| SEQ ID NO 4
| LENGTH: 1065
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                                                                           Length 1065;
                 coding
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                 Sequence:
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; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER PROMATION: Sequence for K2S protein
US-09-987-455-4
                                                                                       red. No. 0;
Mismatches
                                                                           Score 1062;
Pred. No. 0
                                                                        Ouery Match 94.1%; Scc
Best Local Similarity 100.0%; Pr
Matches 1062; Conservative 0;
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967 IGCCAGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG 1026
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121 TCCTGCTGGATTCTCTCTCTGCCGCCCACTGCTTCCAGGAGGTTTCCGCCCCACCACGTG
                                                                   541 GTCGAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
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                                       547 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAA
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Patent No. US20020156263A1

GENERAL INFORMATION:

APPLICANT: Chen, Huel-Mei

TITLE OF INVENTION:

CURRENT APPLICATION UNMBER: US/09/974,298

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 60/238,331

PRIOR PILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 194

SOFTWARE: PROFERMENTE: 2001-10-04

NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.1%; Score 1061.8; Best Local Similarity 99.3%; Pred. No. 0; Matches 1066; Conservative 0; Mismatches
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; LOCATION: 2635
; OTHER INFORMATION: a, t, C,
US-09-974-298-144
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OTHER INFORMATION: Incyte
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US-09-974-298-144
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                                                                                                                                                                                                                                                                                               APPLICANT: Jiridel Manosroi
APPLICANT: Chacchai Tayapiwatana
APPLICANT: Chacchai Tayapiwatana
APPLICANT: Friederich Goetz
APPLICANT: Friederich Goetz
TITLE OF INVENTION: DA-Derived tPA or K2S Molecules
FILE REFRENCE: 0652.2190001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT FILING DATE: 2001-11-14
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2001-02-15
PRIOR PLING DATE: 2001-02-15
PRIOR PLING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 25
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                                                                                                    GITACCAACTACCTAGACTGGATTCGTGACAACATGCGACG 1062
                                                                               GITACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
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94.1%; Score 1062; DB 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                 Sequence 7, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION
APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
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ORGANISM: Artificial Sequence
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US-09-987-455-7
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)
                             Sequence 433, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
    APPLICANT: BERTUCCI; FRANCOIS
; APPLICANT: HOUGATTE, REMI
; APPLICANT: HOUGATTE, REMI
; APPLICANT: HOUGATTE, REMI
; APPLICANT: PRINBAUM, DANIEL
; APPLICANT: PERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT PELLING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PASCENTIN VET: 2.1
; FENCINE OF 433
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Pred. No. 5.9e-62;
0; Mismatches 6; Indels 0;
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US-09-880-503-15
Sequence 15, Application US/09880503
Patent No. US20020131964A1
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; OTHER INFORMATION: a, t, c or
US-10-007-926A-433
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Best Local Similarity 97.4%;
Matches 229; Conservative C
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WANE/KEY: modified base
LOCATION: (57)
OTHER INFORMATION: a, t, c
FEATURE:
COTHER INFORMATION: a, t, c
TEATURE:
NAME/KEY: modified base
LOCATION: (82)
OTHER INFORMATION: a, t, c
FEATURE:
NAME/KEY: modified base
LOCATION: (159)
OTHER INFORMATION: a, t, c
FEATURE:
NAME/KEY: modified base
LOCATION: (159)
OTHER INFORMATION: a, t, c
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OTHER INFORMATION: a, t,
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                           CCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG
                                                                               GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
                                                                                                          GCACGCACAGCCTCACCGAGTGGGTGCTCCTGCCTCCGGTGGAATTCCATGATCCTGA
                                                                                                                                                            TAGGCAAGGTTTACACACACACACACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA
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NAME/KEY: misc feature
LOCATION: 1, 2, 3, 1414, 1415
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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                 APPLICANT: CINES, Douglas B
APPLICANT: CINES, Douglas B
APPLICANT: -, HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE (
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE (
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 1212
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Pred. No. 2.1e-50;
0; Mismatches 459; Indels
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Best Local Similarity 52.3%;
Matches 549; Conservative
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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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APPLICANT: Lillie, James
APPLICANT: Wangyao
APPLICANT: Wangyao
APPLICANT: Wangyao
APPLICANT: Wangyao
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT PAPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR PAPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR SEQ ID NOS: 140084
NUMBER OF SEQ ID NOS: 140084
SEQ ID NO 12748
TGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCAC
                                                                                                                                                                                            ---AATGGAAAACAGA
                                                                                                                                                                                                                                                        963 CGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTT
                                                                                                                                                                                                                                                                                                1026 TICCTGCCAGGGAAACTCAGGGGGACCCCTCGTCTTTTCCCTCCAAGGCCGCATGACTTT
                                                                                                                                                                                                                                                                                                                                                                                        1023 GGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGGTGTGTACAC
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                                                     924 idigiagcidaritcccaccdegagidicageagccccaciaciacaegcrergaagicae
                                                                                                                        CGACAACATGCTGTGCTGGAGACACTCGGAGCGGCGGGCCCCCAGGCAAACTTGCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAGGCAAGGTTTACACAGACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACAT
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                                                                                                                                                                       984 CACCAAAATGCTATGTGCTGACCCCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1083 AAAGGTTACCAACTACCTAGACTGGATTCG 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1146 GAGAGTCTCACACTTCTTACCCTGGATCCG 1175
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1124 CCACTACTACGGCTCTGAAGTCACCACAAAATGCTGTGTGCTGACCCACAGTG--- 1180
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                                                                                                                                                                                                                                                                                                                                                                                    944 TGCGCAGCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGATCCCCA 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1004 GTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGAATTCTACCGACTATCTCTA 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1064 TCCGGAGCAGCTGAAGATGACTGTTGTGAAGCTGATTTCCCACCGGGAGTGTCAGCAGCC 1123
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                                                                                                                                                                                                                                                                                                             699 TGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCC
           585 CGAGGAGGAGCAGAAATTTGAAGTCGAAAATACATTGTCCATAAGGAATTCGATGATGA
                                                                  824 GCAAGGGGAGATGAAGTTTGAGGTGGAAAACCTCATCCTACACAAGGACTACAGCGCTGA
                                                                                                                                                            645 CA-----CTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTG
                                                                                                                                                                                                                                   884 CACGCTTGCTCACCACAACGACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGCCAGGTG
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Fatent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT PILLING DATE: 2001.05-07
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 122
LENGTH: 1475
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llarity 51.3%; Pred. No. 9.6e-44;
Conservative 0; Mismatches 457;
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Best Local Similarity
Matches 551; Conserv
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US-09-850-716A-122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 CCAGCCCTGGTTTGCGGCCATCTACAGGAGGCACCGGGG---GGGCTCTGTCACCTACGT 703
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1132 CAGGCTGACGTGGGAGTACTGTGATGTGGCCTCTGTCACC 1171
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APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: L. Samuel X.
APPLICANT: L. Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Honderson, Robert A.
APPLICANT: Honderson, Robert A.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER; FILE REFERENCE: 210121.455C14
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER; TILLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; TILLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; TILLE OF INVENTION NUMBER: US/09/735,705
CURRENT PILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastERQ for Windows Version 3.0
SEQ ID NO 122
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Pred. No. 9.6e-44;
0; Mismatches 457;
                                                                                                                                                                                        Sequence 122, Application US/09735705 Patent No. US20020052329A1
                                                                                                                                                                                                                                                                                                                                                                            Kalos, Michael D. Bangur, Chaitanya S Hosken, Nancy Fanger, Gary R. Li, Samuel X. Wang, Aijun Skeiky, Yasir A.W.
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Best Local Similarity 51.3%;
Matches 551; Conservative
                                                                                                                                                                                                                                                                                                         Wang, Tongtong
Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C
FILE REPERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 201-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 122
                                                                                                                                                                                      ORGANISM: Homo sapiens
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US-09-897-778-122
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Sequence 122, Application US/09897778
Patent No. US20020147143A1
GENERAL INPORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro

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Search completed: August 19, 2003, 14:22:27 Job time : 320.307 secs
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Publication No. US20030119763A1

GENERAL INROFAMATION:

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121 455C4

CURRENT APPLICATION NUMBER: US/09/466,396A

CURRENT FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 122
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0; Mismatches 457; Indels
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Best Local Similarity 51.3%;
Matches 551; Conservative
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; ORGANISM: Homo sapien
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Scoring table:

Minimum DB Maximum DB

Database

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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: Seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4498.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOBAI021ZDO8_C
$01980 [aciluster=4498.r. Contact : Feng Liang Email :
Eliang@lifetech.com URL: http://fulllength.invitrogen.com/
InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID :
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Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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BQ8699840
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TITLE
JOURNAL
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BX389609 BX389609
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75.6
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AW630119 hh78e06.y AW394127 MR2-TT001 BU190904 AGENCOURT BQ679501 AGENCOURT

EST 01-MAY-2003

895 853 850.2 818.6

Score

Š. Result

83

59

Wed

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/tissue type="dorsal root ganglia"
/devetage="adult, 36 yr"
/lab.host="DH10B"
/clone lib="lungski dorsal root ganglion"
/note="Vector: pcNV-SPORT6 (Life Technologies); Site_1:
/note1; Site_2: Sall; cDNA made by Oilgo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCAGCGCGCGCG-3 and
5'-GACTAGTTCTAGATGCGAGGGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lungki, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
                                                                                                                                                                                                                                                                                                         BU149958 912 bp mRNA linear EST 03-SEP-2002 AGENCOURT 8137213 Lupski dorsal root ganglion Homo sapiens cDNA clone IMAGE:6184119 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LibMA1372 row: m column: 16
High quality sequence start: 18
High quality sequence stop: 644.
AGAACCCCAGTGCCCAGGCACTGGG--CCTGGGCAAACATAATTACTGCCGGAATCCTGA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 912)
MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (
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/clone="IMAGE:6184119"
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TITLE
JOURNAL
COMMENT
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/tissue type="PLACENTA COT 25-NORMALIZED"
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/note="list strand cDNA was primed with a NotI-oligo(dT)
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.

a 268 c 282 g 194 t 2 others
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                                        1. .930
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               Location/Qualifiers
  CS0BAI021ZD08 CS01980
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Matches 912; Conserv
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.ons.fr web: www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
Attps.//www.genoscope.ons.fr
thtp://www.genoscope.ons.fr
cgi-bin/cluster.cgi?seq=CSOBAF025ZG09 AF02376_3&cluster=4498.r.
Contact: Feng Liang Email: fliangelifetech.com URL:
http://tlllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAF025ZG09_AF02376_3.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="PIACENTA COT 25-NORMALIZED"
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/note="ist strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
290 c 277 g 191 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.4%; Score 850.2; DB 13; 96.6%; Pred. No. 1.4e-210; ative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI039YK15"
                                                           Contact: Genoscope
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clone CS0DI039YKIS 5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
                                                                                                                                                                                                                                                                                                                                                                                          GCATGAGGCCTTGTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTA
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                  TGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCCGCAGGCTGACGTGGGGAGTACTG
                                                                               CAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGCAGGCTGCCATCTTTGCCAA
                                                                                                                                                                                                             GCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGCATACTCATCAGCTCCTGCTG
                                                                                                                                                                                                                                                    GCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTG
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Homo sapiens
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180

327 120 387

9

Gaps

240

507 300 567 420

360 627 480 747 807 909

687

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 3 BX389609

ORGANISM

REFERENCE

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BQ278177 993 bp mRNA linear EST 07-MAY-2002
AGENCOURT_7061709 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5805153
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Pred. No. 2.3e-202;
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AGENCOURT 7981262 Lupski_dorsal_root_ganglion Homo sapiens cDNAclone IMAGE:6185661 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                        898
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Vector: pGWV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Contact: Robert Strausberg, Ph.D.
Email: gapba-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:
http://mage.lln.gov
Plate: LiAM13576 row: m column: 22
High quality sequence stop: 665.
                                    TCTCCTTTCTATTCGGAGCGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGC
                                                                                                                                                                                                                                         CCCCTGGTGTGTCTGAACGATGCGCGCATGACTTTGGTGGTGGCCATCATCAGCCTGGGCCTG
                                                                                  TGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGAC
                                                                                                    TGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGAC
                                                                                                                                                     ACTCGGAGCGCCGCGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGC
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6185661"
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BU146167.1 GI:22659699
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BU146167
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Homo sapiens (human)
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NH10B (phage-resistant)"
/clone_lib="NH1 MGC_109;
/note="Organ: overly; Vector: pOTB7; Site_l: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (Dases 1 to 933)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2043 row: o column: 10
High quality sequence stop: 681.
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Pred. No. 4.3e-201;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5805153"
                              BQ278177.1 GI:20488385
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                                                                 sapiens (human)
mRNA sequence.
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BQ690978 8046707 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6209120 AGENCOURT Sequence. 5., mRNA Sequence. BQ690978
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/lab host="DH10B (phage-resistant)"
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/note="Organ: pacreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCGAGG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can by
thtp://image.llnl.gov
thtp://image.llnl.gov
plate: LLCM367 row: o column: 09
High quality sequence stop: 658.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6209120"
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Craniata; Vertebrata; Eutel Catarrhini; Hominidae; Homo

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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
http://www.genoscope.niformation about this cluster, see
http://www.genoscope.niform.fr/
cgi-bin/cluster.cgi?seq=CSOBAF025ZG09 AF02376_2x.
Contact: Feng Liang Email: filang@alfetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAF025ZG09_AF02376_2.
                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertu
Mammalia; Butheria; Primates; Catarrhini; Hoi
1 (bases I to 918)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                       sapiens (human)
                                                                                                                                                                           Contact: Genoscope
                                         Homo sapiens
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                                                                                              71.9%; Score 811.2; DB 13
99.0%; Pred. No. 1.9e-200;
iive 0; Mismatches 8;
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Best Local Similarity 99.0
Matches 816; Conservative
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BX389608
LOCUS
                                     BASE CO
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/tissue type="PIACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
273 c 264 g 186 t 6 others

/organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="CS0D1039xK15"

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                                           Gaps
                                           ë,
71.6%; Score 807.6; DB 13; Length 918; 96.4%; Pred. No. 1.7e-199; ive 0; Mismatches 29; Indels 3;
                                           Matches 855; Conservative
                       Similarity
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918 bp mRNA linear EST 08-MAY-2003 EX389608 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0D1039YK15.5-PRIME, mRNA sequence. EX389608.1 GI:30463469

DEFINITION

ACCESSION VERSION

Gaps

419 120 479 180

9

599

629

539 240

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CGACGCCTGCCAGGCCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGAC 1019
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                                                                                                                GACGTGGGGACTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCA
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                      DB 13;
                                                            Э,
                      Score 796.2; DB 1:
Pred. No. 1.6e-196
                                                         0; Mismatches
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                                                         Matches 820; Conservative
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/lab_host="blub" (phage-resistant)"
/clone_lib="NIH MGC_109"
/note="forgan: ovary; vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRAL/AhoI sites using the following 5' adaptor:
GGCACGACGA(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

L (basea 1 to 930)

S NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2780 row: g column: 13
High quality sequence stop; 639.
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AGENCOURT 10412263 NIH MGC 109 Homo sapiens cDNA clone IMAGE:6578533 5', mRNA sequence.
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/mol type="mRNA"
/do _ref="texaon:9606"
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/clone lib="NIH
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                                                                                                                     Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llni.gov
Plate: LLCM2316 row: e column: 21
High quality sequence stop: 630.
High quality sequence stop: 630.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_8775988 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:63734895027899.1 GI:22342930
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/tissue Lype="large cell carcinoma"
/tissue Lype="large cell carcinoma"
/lab_host="DH108 (plage-resistant)"
/clone lib="NH108 (plage-resistant)"
/clone lib="NH108 (plage-resistant);
/clone lib="Organ: lung; Vector: poTB7; site 1: XhoI; Site 2:
EcoRI; coDAM made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Barkeley) using ZAP-CADA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                              780
                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCACGACGCCT-GCCAGGGCGATTCGGGAGGCCCCCTGGT-GTGTCTGAACGATGG-C 1011
                                     540
                                                                                777
                                                                                                                       900
                                                                                                                                                                 837
                                                                                                                                                                                                                                                  897
                                                                                                                                                                                                                                                                                         720
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                     GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCCGCTGTGCCCCAGGAGAGCAGCGTG
                                                                                                      GTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCCGGACTGCCGGACTGGAGTGTGAG
                                                                                                                                                                                         GTCACCGACAACATGCTGTGGTGCTGGAGACACTCGGGAGCGGCGGGGCCCCCCAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACA
GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCCGCTGTGCCCAGGAGAGCAGCGTG
                                                                                GTCCGCACTGTGTGCCTTTCCCCCGGCGGACCTGCAGCTGCCGGACTGAGAGGAGTGTGAG
                                                                                                                                                                 CTCTCCGGCTACGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAG
                                                                                                                                                                                                                                                                            GCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTACTTAACAGAACA
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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/dlone lib="NHH MGC 116"
/note="Organ: pooled colon, kidney, stomach; Vector:
powd-SPORTS; Site=1: Not!; Site=2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases lto 510, mgc.)

I (bases lto 510, mgc.)

INIH-MGC http://mgc.nci.nih.gov/.

INIH-MGC http://mgc.nci.nih.gov/.

INIH-MGC http://mgc.nci.nih.gov/.

INIH-MGC http://mgc.nci.nih.gov/.

INIH-MGC http://mgc.nci.nih.gov/.

Insue procurement: Life Technologies, Inc.

CONTACL: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://maga-llh.gov

Righ quality sequence stop: 837.

I cation/Qualifiers

Location/Qualifiers
                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TACAGCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCATACTCATCAGCTCCTGCTGGATTCTCTGCCGCCCACTGCTTCCAGGAGGTTT
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Pred. No. 3.1e-188;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5190556"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
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ilarity 99.7%;
Conservative 0
     Homo sapiens (human)
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Best Local Simil
Matches 776; C
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AUTHORS
TITLE
JOURNAL
COMMENT
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BI765247.1 GI:15756825
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                                                                                                              Gaps
                                                                                                              3,
                                                                           Length 950;
                                                                                                                                                 CCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCT
                                                                       Score 765.2; DB 13; Length
Pred. No. 2e-188;
0; Mismatches 13; Indels
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                     ı
                     181
               279 g
NIH MGC Library
                                                                     Query Match
Best Local Similarity 98.1%;
Matches 806; Conservative
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BG763582 958 bp mRNA linear EST 15-MAY-2001
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                                                                                             CGAGTCGGTCCTCCTCCCCGGTGGAATTCCATGATCCTGATAGGCAAGGTTTAC
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                                                                            GGGAAACAGTGACTGCTACT - TTGGGAATGGGTCAGCCTACCGTGGCACGCACGCACACCACG
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   DB 10;
 Score 706.8; DB 10;
Pred. No. 3.2e-173;
0; Mismatches 52;
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BG763582.1 GI:14074235
Query Match
Best Local Similarity 93.3%;
Matches 793; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_39"
/clone_lib="NIH MGC_30"
/note="Organ: pancress; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI, CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis Xit (Stratagene) and Superscript II RT (Life
                                                                                                                                                                                                                                                                                                                                                                                            GGTGTGTACACCAAGGTTACCAACTACCTAGACTTGGATTCGTGACAACATGCGACCG 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The TINCYTE Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LiCM267 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 759.
                     TGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCTCTTCTATTCGGAGCGCCTG
                                                                                             AAGGAGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAAC
                                                                                                                                                                      AGAACAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGCCCCCAGGCA
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                                                                          AAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACACATTTACTTAAC
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BE616613

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FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

12 1 (bases 1 to 974)

13 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lu Onpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIALI)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLCAN2645 row: a column: 06

High quality sequence stop: 603.

Location/Qualifiers
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/tissue_type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_line="NHH-MGC_101"
/note="Organ: liung, Vector: poTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRIXhol sites using the following S' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
                                                                                                                                                                                                                                                                                                                                    721 GGTGGTCCGCACTGTGTGCCTTTCCCCCCGGCGACCTGCAGCTGCGGACTGGACTGGACGGA 780
                                                                                                                                                                                                                                       661 ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCCGGTGTGCCCAGGAGAGCAGC
                                                                                 CCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC
                                                                                                                                       596 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGACACTTACGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6459629"
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                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 958)
                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLCM1719 row: n column: 21
High quality sequence stop: 810.
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Pred. No. 1.5e-171;
0; Mismatches 41; Indels 15; Gaps
                                                                                             NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity 93.8%;
Matches 840; Conservative
  Homo sapiens (human)
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                      Homo sapiens
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(MGC)

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 709) NHH-MGC http://mgc.nci.nih.gov/.

Unpublished

REFERENCE AUTHORS TITLE JOURNAL COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence start: 3

High quality sequence stop: 701.

/organism="Homo sapiens"
/mol type="manNa"
/db xref="texon:9606"
/clone="IMAGB:3925600"
/tissue type="choriocarcinoma"
/lab\_host="DH10B (phage-resistant)"
/clone\_lib="NIH\_MGC\_21"

source

FEATURES

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Berkeley) using ZAP-cDNA synthesis kit
Superscript II RT (Life Technologies).
NIH_MGC Library."
7.23 c 279 g 187 t
                                                                                                       Score 694.4; DB 13;
Pred. No. 5.5e-170;
0; Mismatches 11;
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/note=Torgan: placenta, Vector: pOTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAGG(G). Size-selected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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BE732704
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682

420 742 480

BE732704.1 GI:10146696

sapiens (human)

Ношо

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

ACCESSION

BE732704 LOCUS

Homo sapiens

322

Gaps

9

382

CGGACCTGCAGCTGCCGGACTGGAGCTGTGAGCTCTCCGGCTACGGCAAGCATGAGG 802	CGGACCTGCAGCTGCACGGACGGAGGGTGTGTGTTTTTTTT	CCTTGTCTTCTTTCGGAGGGGCTGAAGAGGCCTCATGTCAGACTGTACCCATCCA 862	CCTIGICCCCTITCTATICGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCA 600	GCCGCTGCACATČACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGTG	GCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGTG	GAGACACTCGGAGCGGCCCCCAGGCAAACTTGCACGACGCCTGC 969	GAGACACTCGGAGCGGCGGG-CCCAGGCAAACTTGCACGACGCCTGC 706
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Search completed: August 19, 2003, 08:29:18 Job time: 3300.95 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model	August 18, 2003, 19:53:48; Search time 4736.31 Seconds (without alignments) 9743.047 Million cell updates/sec	US-09-987-455-2 1128 1 atgaaaaagacagctatcgcttcgtgacaacatgcgaccg 1128	IDENTITY NUC Gapop 10.0 , Gapext 1.0
OM nucleic - nu	Run on:	Title: Perfect score: Sequence:	Scoring table:

5777422 Total number of hits satisfying chosen parameters: 2888711 segs, 20454813386 residues Minimum DB seq length: 0 Maximum DB seq length: 200000000 Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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9b om: \*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AX431268 Sequence AX431271 Sequence A27435 DNA sequenc	E01937 Synthetic D A30593 DNA for tis	AR059996 Sequence E01944 Synthetic D	106609 Sequence 44 106614 Sequence 46	108789 Sequence 3 A06611 Synthetic n	A10226 Synthetic D E01176 DNA encodin	101581 Sequence 1	101256 Sequence 3	rtili Lapien	A27429 cDNA sequen E01934 DNA encodin	AR059986 Sequence	-	AR017931 Sequence 118796 Sequence 3		DNA enc	IO7841 Sequence 1 IO7989 Sequence 1	109622 Sequence 1	E01055 DNA encodin A01465 H. Bapiens t	I08638 Sequence 2	108637 Sequence 1	7	A14927 tPA-DNA fro	204	205	8 DNA encod 3 DNA encod		. linear PAT 28-JUN-2002			Manosroi,A. and Manosroi,J. ecombinant dna-derived tpa	
SUMMERTES	ID	3126 3127 435	E01937 A30593	AR059996 E01944	106609 106614	108789 A06611	A10226 E01176	101581	101256	A07197	A27429 E01934	AR059986	AR017909	AR017931 118796	A07209	E01163	I07841 I07989	109622	E01055	108638	108637		A14927	A34204	A34205	E02448 E02663	ALIGNMENTS	1128 bp DNA	6150	ū	., Tayapiwatana,C., ale production of r	4 2 23-MAY-2002;
d	Query Match Length DB	00.0 1128 00.0 1128 94.4 1314	.4 1314 .4 1341		.4 1689	.4 1689	.4 1780	.4 1836	.4 1989	.4 2099	.4 2100	.4 2101	.4 2151	.4 2162	.4 2249	.4 2547	.4 2547	.4 2547	.4 2549	.4 7533	.3 1689	.3 1506	.3 1689	.3 1689	.3 1689	.3 1689 .3 1689		131268 Tuence 2 from Patent	AX431268.1 GI:21656	<pre> introductio construct synthetic construct artificial sequences</pre>	Wer ecu	Patent: WO 0240650-A
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                                                                               OmpA-K2S fusion protein"
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                                                                                                                                 Length 1128,
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Pred. No. 5.5e-259;
Mismatches 0;
GER INGELHEIM INT (DE)
Location/Qualifiers
1. 1128
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xrefe="taxon:32630"
/note="coding sequence for OmpA-%
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Best Local Similarity 100.
Matches 1128; Conservative
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<b>&amp;</b> 8	901 ACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGCGCCCCAGGCAACTTGCAC 960 
oy Pp	961 GACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCATGACT 1020
oy op	1021   TTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTAC   1080
& A	1081 ACAAAGGTTACCAACTAGACTGGATTCGTGACAACATGCGACG 1128 
RESULT 2 AX431271 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	AX431271 1128 bp DNA linear PAT 28-JUN-2002 N Sequence 5 from Patent WO0240650. AX431271 AX431271.1 GI:21656153
SOURCE ORGANISM REFERENCE	<pre>synthetic construct I synthetic construct artificial sequences.</pre>
AUTHORS	IORS Goetz, F., Werner, R.G., Tayapiwatana, C., Manosroi, A. and Manosroi, J. B. Methods for large scale production of recombinant dna-derived tpa or k2s molecules
FEATURES SOURC	BOEHRINGER INCELHEIM INT (DE)  Location/Qualifiers
BASE COUNT ORIGIN	/note="coding sequence for OmpA-K2S rusion protein 238 a 332 c 332 g 226 t
Query Match Best Local S Matches 1128	<pre>atch</pre>
Vo da	1 ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGG
yo, da	61 GCGGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACG 120
8 8	121 CACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCGTGGAATTCCATGATCCTGATAGGC 180
i o qa	AAGGITTACACAGCACAGAACCCCAGTGCCCAGGCCTTGGGCAAACATAATTAC 24 
ò a	241         TGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTG         300           241         TGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTG         300
රු සි	301 ACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGCCCTGAGACAGTACAGCCAG 360 101 ACGTGGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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Match 94.4%; Score 1065; DB 6;	Hest Local Similarity 99.5%; Pred. No. 6.5e-244; Matches 1068; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Ov 56 CCCAGGGGGTTGTGAGGGAAACAGTGACTTTGGGAAATGGGAAATGGGGAAATGGGGAAATGAGTTACTTTTGGGAAATGGGGAAATGAGTTTTGGAAAATGAGTTACTTTTGAAAAAGAGTAGATGACTTTTTGGAAAATGAGTTACTTTTGAAAAAAGAGTAGAAATGAGTTACTTTTAGAAAAAAAGAGTAGAAATGAGAAAAAGAGAAAAGAAAAAGAAAAAA	239 CCCTGCCTCCTCTGAGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG 29	Qy 116 GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTGGAATTCCATGATCCTGA 175	QY 176 TAGGCAAGGTTTACACAGGCACCAGGCACTGCCCAGGCACTGGGCCTGGGCAACATA 235	Oy 236 ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCTGAAGAACCGCA 295	Qy         296         GGCTGACGTGGGATACTGTGATGTGCCCTCCTGCTCCACCTGCGCCTGACACAGTACA         355           Db         479         GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA         538	Qy 356 GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC 415	Oy 416 AGGCTGCCATCTTTGCCAAGCACGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGCA 475	Oy 476 TACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGACGTTTCCGC 535	Qy         536         CCCACCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGGAGC         595           1	Qy 596 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA 655	OY 656 ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCG 715	Qy         716 TGGTCCGCACTGTGCCTTCCCCGGCGACCTGCAGCTGCCGGACTGGACGGAGTGTG         775           Db         899 TGGTCCGCACTGTGCCTTCCCCCGGACCTGCAGCTGGACTGGACGGAC	836 AGGCTCATGTCAGACTGTACCCATCCAGCGCTGCACATCACAACATTAACTGAAA B	Qy         896         CAGTCACCGACAACATGCTGTGCTGGAGACACTCGGAGCGGGGGCGGGC	OY 956 TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTCTGGACGATGGCCGCA 1015	QY         1016         TGACTTTGGTGGGCATCATCACTGGGGCCTGGGCTGGACAGAAGATGCCCGGGTG         1075
Db 361 CCTCAGTTTCGCATCAAAGGAGGTCTTCGCCGACATCGCCTCCCACCCTGGCAGGCT 420 Qy 421 GCGATCTTTGCCAAGGAGGTCGCCGGAGAGAGGGGTTCCTGTGCGGGGGGATACTC 480		481 ATCAGCTCCTGCTGCTGCTCTCTCTCTGCCGCCCACTGCTTCCAGGAGAGTTTCCGCCCCAC	Qy 541 CACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGCAGAAAA 600	OY 601 TTTGAAGTCGAAAATACATTGTCCATAAGGAATTCGATGATGACATTACGACAATGAC 660 	QY         661 ATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGAAGCAGCGTGGTC         720           Db         661 ATTGCGCTGCTGCAGCTGAAATCGACCCGCTGTGCCCAGAAGAGCAGCGTGGTC         720	Qy         721         CGCACTGTGTGTGCTTCCCCGGCGGACTGCCGGACTGGACGGAC	OY 781 TCCGCTACGCCAACCATGAGGCCTTGTCTCTATTCGGAGCGCTGAAGGAGGCT 840	OY 841 CATGTCAGACTGTACCCATCCAGCGCTGCACATCACAACATTTACTTAACAGAACAGTC 900	OY 901 ACCGACAACATGCTGTGCTGGAGACACTCGGAGCGGCGGCCCCCAGGCAAACTTGCAC 960 	Oy 961 GACGCCTGCCAGGCGATTCGGGAGGCCCCTGGTGTCTGAACGATGGCCGCATGACT 1020	QY         1021         TTGGTGGGCATCATCACAGGGCCTGGGCTGTGGACGATGTCCCCGGGTGTGTAC         1080           Interpretation         1021         TTGGTGGGCATCATCACTGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTAC         1080	OY 1081 ACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACGG 1128 	RESULT 3 A27435 LOCUS A27435 LOCUS DEFINITION DNA sequence of coding region in pTQkPadeltatrp. ACCESSION A27435 VERSION A27435	KEYWORDS . SOURCE synthetic construct ORGANISM synthetic construct artificial sequences.	REFERENCE 1 (Dases 1 to 1314) AUTHORS Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and Kobayashi,M. TITLE New tissue plasminogen activator	WAL SS Surc	/organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630" BASE COUNT 286 a 393 g 249 t

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1019 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACACATCACAACATTAACTTAACAGAA 1078
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959 AGCTCTCCGGCTACGCCAGCATGAGGCCTTGTCTTCTATTCGGAGCGGCTGAAGG
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                                                                                                                        539 GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGC
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synthetic construct

synthetic construct

artificial sequences.

1 (bases 1 to 1314)

RS Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and

Kobayashi,M.

NOVEL 11919

Artificial sequence; Genes.

PATOTICANA PHARMACEUT CO LTD

OS Artificial sequence; Genes.

PNOVEL 11989104167-A/4

PD 21-APR-1989

PF 01-AUG-1987 GB 87 8718298, 26-OCT-1987 GB.87 8725052, PR

PN 1989104167-A/4

PD 21-APR-1989

PF 01-AUG-1987 GB 87 8718298, 26-OCT-1987 GB.87 8725052, PR

PN 1989104167-A/4

PN 21-APR-1989

PF 01-AUG-1987 GB 87 8718298, 26-OCT-1987 GB.87 8725052, PR

PN NTWA MINEO, SAITO YOSHIMASA, SASAKI HITOSHI, HAYASHI MASAKO, PI NOTANI JOJI, YOSHIMASA, SASAKI HITOSHI, HAYASHI MASAKAZU

PT NTWA MINEO, SAITO YOSHIMASA, SASAKI HITOSHI, HAYASHI NOTANI JOJI, PI NOTANI JOJI, CC CLISNI/64, CIZNI/20, CLISNI/00, CLIZNI/64, CLIZNI/19);

CC CLISNI/64, CLIZNI/20, CLIZNI/00, CLIZNI/64, PC CLIZNI/64, CLIZN
                                                                                                                                                                            EUL937 1314 bp DNA linear PAT 29-SEP-1997
Synchetic DNA encoding new t-PA tissue plasminogen activator.
E01937
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                                                    1259 TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1311
                           TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
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99.5%; Pred. No. 6.5e-244;
ive 0; Mismatches 5;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
386 c 393 g 249 t
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/product='t-PA'
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JP 1989104167-A/4.
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Best Local Similarity 99.5
Matches 1068; Conservative
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838 715 898 775 958 835 1015 1198 1075 A30593 1341 bp DNA linear PAT 04-AUG-1995 DNA for tissue plasminogen activator (t-PA) from patent BP0400545. A30593 GI:1249165 synthetic construct
synthetic construct
synthetic construct
artificial sequences.
1 (base 1 to 1341)
Stern, A., Kohnert, U., Rudolph, R., Fischer, S. and Martin, U.
Parivative of tissue plasminogen activator
Patent: EP 0400545-A 2 05-DEC-1990;
BOEHRINGER MANNHEIM GMBH
Location/Qualifiers

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09-JUL-2002
                1016 TGACTTTGGTGGGCTCATCAGCTGGGGCCTGTGGACAGAAGGATGTCCCGGGTG
1229 TGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCCTGTGGAAGAAGATGTCCCGGGTG
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                                                                   TGTACACAAAGGTTACCAACTACATAGATTCGTGACAACATGGGACCG
                                                                                                                                                                  PAT
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synthetic construct
artificial sequences.
1 (Separation 1419)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and
Kobayashi,M.
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Patent: BP 0302456.A 49 08 FEB-1989;
FUJISAMA PHARMACEUTICAL CO., LTD
Location/Qualifiers
1. 1419
/ organism="synthetic construct"
/ mol type="genomic DNA"
/ db xref="ason:32630"
309 a 413 c 426 g 271 t
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Pred. No. 6.5e-244;
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A27725.1 GI:21727236
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99.5%;
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                                                                                Score 1065; DB 6;
Pred. No. 6.5e-244;
0; Mismatches 5;
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
397 c 399 g 252 t
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larity 99.5%;
Conservative
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Matches 1068; Conserv
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115 403 175 463 235 523 295 355

643 415 703 475 763 535 823 595 883

Db   464 TAGGCAAGGTTTACACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAACATA 523   236 ATTACTGCCGAATCCTGATGGGAATGCCAGCCCTGGTGCCAGTGCCAGTGCTGAAGAACGCA 295	416 AGGCTGCCATCTTTGCCAAGCACAGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGCA 4	DD   824 CCCACCACCTGACGGTGATCTTGGGCAGACATACCGGGTGGTCCCTGGCGAGGGGGC   883	776 AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTTCTTTTCTATTCGGAGCGGCTGAAGG 8	Qy         1076 TGTACACAAGGTTACCAACTACCTAGACTCGACAACATCGGACCG         1128           Db         1364 TGTACACAAAGGTTACCAACTACCTAGACTCGGACTGGACACTGCGACCG         1416           RESULT         8           RESULT         8           DEPINITION         Synthetic DNA encoding new t-PA tissue plasminogen activator.           ACCESSION         E01944           VERSION         E01944           ACCESSION         E01944           VERSION         E01944           VERSION         E01944           VERSION         E01944           VERSION         F01944           VERSION         F01944           VERSION         F01944           VERSION         F01944           ACCESSION         F01944           VERSION         F01944           ACCESSION         SUBSION-F016-F016-F016-F016-F016-F016-F016-F016
596 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA 65	Qy         776 AGCTCTCCGGCTAGGGCATGGTCTTCTATTCGAAGGGGTGAAGG 835           bb         1064 AGCTCTCCGGCTAGGGCAAGCATGAGGCCTTTCTATTCGAAGGGTGAAGG 1123           Qy         836 AGGCTCATGTACCCATCCAGCGCTGCTCCTTTCTATTCGAAGGTGAAGG 1123           Qy         836 AGGCTCATGTACCCATCCAGCGCTGCACACATTTACTTAACAGA 895           Db         1124 AGGCTCATGTCAGACTGTACCCATCCAGCGCTGCACATCACACATTTACTTAACAGA 1183           Qy         896 CAGTCACCGACAACATGTGTGCTGGAGACACTCGGAGGGCCCCAGGCAAACT 955           P	Qy         956 TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCTGGTGTCTCTGAACGATGGCCGCA 1015           bb         1244 TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTCTTGAACGATGGCCGCA 1303           Cy         1016 TGACTTTGGTGGCATCATCAGCTGGGCCTGGGCTGTGGACAACGAAGGATGCCCGGGTG 1075           Db         1304 TGACTTTGGTGGCATCATCAGCTGGGCCTGGGCTGTGGACAACGAAGGATGCCCGGGTG 1363           Qy         1076 TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128           Db         1364 TGTACACAAAGGTTACCAACTAGACTGGATTCGTGACAACATGCGACCG 1416	AR05996	Query Match         94.4%;         Score 1065;         DB 6;         Length 1419;           Best Local Similarity         99.5%;         Pred. No. 6.5e-244;         0;         Gaps         0;           Matches 1068;         Conservative         0;         Mismatches         5;         Indels         0;         Gaps         0;           Qy         116

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655 943 715

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1004 TGGTCCGCACTGTGTGCCCTTCCCCCGGCGAACTGCAGCTGCCGGACTGGACGGAGTGTG 1063
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944 ATGACATTGCGCTGCTGCAGCTGAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCG
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                                             596 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA
                                                                                                   656 ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCG
                                                                                                                                                            716 TGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTG
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Mulvhill,E.R., Nexo,B.A., Yoshitake,S., Ikeda,Y., Suzuki,S.,
Hashimoto,A. and Yuzuriha,T.
Mutant t-PA with Kringle replacement
Patent: EP 0293934-A1 44 07-DEC-1988;
Location/Qualifiers
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Pred. No. 6.5e-244;
0; Mismatches 5;
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Best Local Similarity 99.5%;
Matches 1068; Conservative
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1 (bases 1 to 1419)
Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J.
Kobayashi,M.
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99.5%; Pred. No. 6.5e-244;
iive 0; Mismatches 5;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Suzuki, S.

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Mulvihill, E.R., Nexo, B.A., Yoshitake,
Hashimoto, A. and Yuzuriha,T.
Mutant t-PA with Kringle replacement
Patent: EP 0293934-Al 46 07-DEC-1988;
Location/Qualifiers
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106614 1689 bp 1 Sequence 46 from Patent BP 0293934. 106614 GI:590640 Unknown

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Qy         896 CAGTCACCGACAACATGCTGTGTGTGTGTGTGTGGAGCCGCGGGCCCCAGGCAAACT         955           Db         1454 CAGTCACCGACAACATGCTGTGTGTGTGTGTGTGTGTGTG	00789 69789 08789 08789 1 GI:588494 08789.1 GI:588494 08789 08789 088888 0 Classified. 08888 0 Classified. 1 Classified. 1 1689 1 1689 1 1689 1 1689 1 1689 1 1689 1 1689	Query Match         94.4\$; Score 1065; DB 6; Length 1689;           Best Local Similarity         99.5\$; Pred. No. 6.5e-244;           Matches 1068; Conservative         0; Mismatches         5; Indels         0; Gaps         0;           Qy         56 CCCAGGGGGCCTGAAGGAAACAGTGACTGCTACTTTGGGAATGGGTCACCTACCT	236 ATTACTGCCGGAATCCTGATGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGACCGCACGTGTGTGAAGACCGCAAGCCCTGGTGCCACGTGCTGAAGACCCGCAAGCCCTGGTGCCACGTGCTGAAGACCCGCAAGCCCTGGTGCCACGTGCTGAAGACCCGCAAGCCCTGCTGCTGCTGAAGACCCGCAAGCCCTGCTGCTGCTGAAGACCCGTACAAGCCCTGCTGCTGCTGCTGACAGTACAAGCACTGCTGCTGCTGCTGCTGCTGACAGTACAAGCCCTCCTGCTGCTGCTGCTGCTGACAGTACAAGCTGCTCTTGCCACCTTGCTGATGTGCCCTCCTGCTCCTGCTGCTGCTGACAGTACAAGAAGAGAGGCTCTTCGCCGAACATCGCCTCCCACCCCTGGCCTGGCCTGGCCTTGCCAAGCACACACA

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/transl_table=11
/product="mutent tissue plasminogen activator (t-PA)"
/product="mutent tissue plasminogen activator (t-PA)"
/protein_id="CAA00883.1"
/protein_id="C1:4906583.1"
/translation="MAAMKAGE"
/translation="MAAMKAGE"
/translation="MAAMKAGE"
/translation="MAAMKAGE"
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YSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYVFKAGKYSSEFCSTPACSEGNSDCYFG
NGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKP
WCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAIFARRRR
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IVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYG
KHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDA
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                                                        TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA
                                                                                         1530 TGCACGCCTGCCAGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCA
                                                                                                                                                                       1016 TGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCCGGGTG
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synthetic construct
artificial sequences.

1 (bases 1 to 1780)
Petersen,L.C. and Boel,E.
A tissue plasminogen activator analogue
Retent: EP 0351246-A 7 17-JAN-1990;
NOVO-NORDISK A/S; NOVO NORDISK A/S
Location/Qualifiers
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Pred. No. 6.5e-244;
0; Mismatches 5;
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misc_difference 1367. 1372
misc_difference 1367. 1369
misc_difference 1367. 1369
//note="in t-PA CR19S, K419S"
//note="in t-PA C87S, K419S"
//replace="in t-PA C87S, K419S"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 99.5%;
Matches 1068; Conservative
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Synthetic DNA for mut
A10226
A10226.1 GI:490657
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884835 PI SHIYOUGUANGU RIN

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12. .1793
/product='this-kringle plasminogen activator'
12. .71
/product='signal peptide of urokinase' PT
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                                                                                                                                                        14-AUG-1985 US 85 766163, 11-JUL-1986 US 86 POOUEN HANGU, NARENDAA KUMAARU KARUYAN, PI
                                                                                                                                                                                                       CIZNO (52.CIZR1:19), (CIZNIS/00,CIZR1:19);
strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
*source: cell type=fibroblast;
*source: cell Location/Qualifiers
Key
          synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 1836)
Pooru, P.H., Narendaa, K.K. and Shiyouguangu, R.R.
POLYCLINGLE PLASMINOGEN ACTIVATING FACTOR
AMERICAN HOME PROD CORP
                                                                                                                                                                                                                                                                                                                                                                            Artificial gene
Artificial sequence; Genes.
homo sapiens
JP 1987104577-A/1
15-MAY-1987
                                                                                                                                             13-AUG-1986 JP 1986191173
14-AUG-1985 US 85 7661
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Best Local Similarity
Matches 1068; Conserv
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GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
                                                             ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCA
                                                                                                    GCCTGACGTGGGAGTACTGTGATGTGCCCTTCCTGCTCCACCTGCGGCCTGAGACAGTACA
                                                                                                                  GCTGACGTGGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGGGGCCTGAGACAGTACA
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product='this-kringle plasminogen activator'

GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA 1017 415 115 175 AGGCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCA 475 777 837 235 897 295 957 GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA 355 838 TAGGCAAGGTTTACACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCCAAACATA 898 ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCA CCCAGGCGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG cccrcccrccrccrcagagaaacacrccracracrrraggaaraggrcagccraccar 116 GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCTCCTGAATTCCATGATCCTGA GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTCCCGTGGAATTCCATGATCCTGA TAGGCAAGGTTTACACACAGAACCCCAGTGCCCCAGGCACTGGGCCTGGGCAAACATA ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCA GCCAGCCTCAGTTTCGCATCAAAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGC ; 0 Length 1836; Indels Score 1065; DB 6; Pred. No. 6.5e-244; 0; Mismatches 5; 94.4%; ilarity 99.5%; Conservative 0 356 1018 416 g 8

29-SEP-1997

PAT

linear

E01176
1836 bp DNA linea
DNA encoding tris-kringle plasminogen activator.
E01176.1 GI:2169435

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B 1 (bases 1 to 1836)
S. Hung, P. P., Kalyan, N.K. and Lee, S.-g.L.
Poly-kringle plasminogen activator
AL Patent: US 4916071-A 1 10-APR-1990;
American Home Products Corporation; New Yor
ES Location/Qualifiers
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Human tPA clone.		d pKG12	Entire sequence of	Plasmid pEMp1-tPA.		Novel plasminogen	Glycosylated plasm	Sequence encoding	Sequence encoding	Tissue type plasmi	Tissue plasminogen	Mutated t-PA analo	Part of tPA024 gen	<b>EPA023</b>		T-PA67+ mutant wit	Human tissue plasm	Full-length tissue	Human tissue plasm	Sequence encoding	T-PA variant contg	Plasmid plgNTQTPA	T-PA with -ve char	Sequence encoding	Human tissue plasm	Plasmid plgN delta	Sequence encoding	cDNA sequence enco	cDNA of human tiss	Human tissue plasm	Human tissue type	Sequence encoding	DHFR/intron (WTras	$\boldsymbol{\vdash}$	Sequence of coding	
AAQ87370 AAV37294	K	AAN90542	AAN70491	AAN81970							-	AAN81090	AAQ04903							AAN60700	AAQ12073	AAQ05534	AAQ12072	Ø,		AAQ05535	AAQ05944	4			ABL59544	AAN30001	AAT15930	AAD40616	AAN91120	
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e 5	11		13			16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

RESULT 1

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Tissue plasminogen activator; tPA; kringle 2 serine protease; stroke; KSS; cardidac inferaction; acute mycocardial infarction; bulmonary embolism; artery occlusion; deep vein thrombosis; blood clotting; thrombolytic; cerebroprotective; cardiant; ompA; fusion protein; gene; ds.
                                                                                                                                                                                              Location/Qualifiers
1..1128
/*tag= a /rtag= a /product= "OmpA-K2S fusion protein"
/product = "OmpA-K2S fusion protein"
/transl except= (pos:1126..1128, aa:Pro-Gly)
/note= "No stop codon"
                                                                                  OmpA-K2S fusion protein encoding DNA.
           BP.
           AAD40614 standard; DNA; 1128
                                                           (first entry)
                                                                                                                                                                                                                                                                         /partial
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                                                                                                                                                                        Unidentified
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                                    AAD40614;
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AAD40614
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07-NOV-2001; 2001WO-EP12857

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TTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGAC
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plasminogen; vascular diseases.
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87GB-0025052.
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13-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method of producing extracellularly secreted, active, correctly folded, recombinant tissue plasminogen activator (tPA). Kringle 2 serine protease molecule (KSS) or their variants in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal peptide OmpA. The method is useful for producing recombinant DNA-derived tPA, K2S or their variants. Sequences of the invention are useful for manufacturing a medicament for treating stroke, cardiac infarction, acute myocardial infarction, pulmonary embolism, any artery occlusion such as intracranial artery occlusion (e.g., arteries supplying the brain), peripherally occluded arteries, coronary artery occlusion, deep vein thrombosis or related diseases associated with unwanted blood clotting. The present sequence is a DNA encoding a fusion protein comprising OmpA and K2S protein.
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                                                                                                                                                                                      Producing active, correctly folded recombinant tissue plasminogen activator, Kringle 2 serine protease in prokaryotic cells by expressing the protein-encoding DNA operably linked to DNA coding for signal
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iive 0; Mismatches 0;
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14-NOV-2000; 2000GB-0027779
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                                                                                                            1139 TGCACGACGCCTGCCAGGCGATTCGGGAGCCCCCCTGGTGTGTCTGAACGATGGCCGCA
                                                                                                                                                                                             1199 TGACTTTGGTGGGCATCATCAGCTGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTG
                                               CAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGCGCCCCAGGCAAACT
                                                                                                                                                                          1016 TGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGGTG
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                                                                                                                                                                                                                                      This sequence encodes a non-glycosylated tPA deriv. lacking the finger- and EGF-domains. The polypeptide has a lower clearance rate (longer half-life) than natural tpA while retaining thrombolytic activity and stimulation by fibrin. (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New non-glycosylated form of tissue plasminogen activator - with thrombolytic activity and long plasma life
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Pred. No. 3.9e-225;
0; Mismatches 5; IndelB 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue plasminogen activator; thrombolysis; finger domain;
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Best Local Similarity 99.5%;
Matches 1068; Conservative
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31-MAY-1989;
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                                                                           New tissue plasminogen activator - comprising finger and growth factor domains lacking tPA longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                      Sequence 1314 BP; 286 A; 386 C; 393 G; 249 T; 0 other;
Sasaki H, Hayashi M, Notani J,
                                                                                                                                                                      on 03-OCT-2002 to add missing OS field.) on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                   Query Match 94.4%; Score 1065; DB 10;
Best Local Similarity 99.5%; Pred. No. 3.9e-225;
Matches 1068; Conservative 0; Mismatches 5;
                                                                                                                                         Disclosure; Page ?; 68pp; English.
                               WPI; 1989-040625/06.
P-PSDB; AAP94409.
Saito Y,
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                                                                                                                                      Tissue plasminogen activator; tPA; thrombolytic agent;
plasminogen; vascular diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1419 BP; 309 A; 413 C; 426 G; 271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                            New tissue plasminogen activator - comprising finger and growth factor domains lacking longer half-life and stronger thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on 03-OCT-2002 to add missing OS field.) on 25-MAR-2003 to correct PA field.)
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99.5%; Pred. No. 3.9e-225;
tive 0; Mismatches 5;
                                                                                                               coding region in plasmid pmTQk112
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                                                                                                                                                                                            Location/Qualifiers
1..1065
/*tag= a
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                    BP.
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                     1419
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87GB-0025052.
87GB-0026683.
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                                                                 (updated)
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(first entry)
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Matches 1068; Conservative
                     DNA;
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P-PSDB; AAP94416.
                    standard;
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26-OCT-1987;
13-NOV-1987;
                                                                 25-MAR-2003
03-OCT-2002
18-JUN-1990
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                                                                                                                                                                                                                                   One N-glycosylation site, i.e. NSS (117-119) is substituted with NSM and the N-glycosylation is removed.
Plasmid encoding the modified tPA is 99-6300 and its transformant is E.coli RR1.Zem 99-6300 (FERM P-9127).
This modified tPA, used to treat thrombosis, is of high quality and has a longer half life period in blood.
See also AAN82177-N82179.
(Updated on 10-MAR-2003 to correct PF field.)
(Updated on 25-MAR-2003 to correct PF field.)
(Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 1689;
                                                                                                                                                                              Modified tissue plasminogen activator - having glycine-183 residues sustd. with serine and threonine.
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 1065; DB 9
Pred. No. 4e-225;
0; Mismatches
                                                                                                                                                                                                                  Disclosure; Page ?; 16pp; Japanese.
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Best Local Similarity 99.5%;
Matches 1068; Conservative
                                                                      87JP-0064339
                                                                                                                    CO LTD
                                                                                                                                         WPI; 1988-311961/44.
P-PSDB; AAP82581.
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                                                                      20-MAR-1987;
                                              26-SEP-1988
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                       GCCAGCCTCAGTTTCGCATCAAAGAGGCTCTTCGCCGACATCGCCTCCCTGGC
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03-NOV-1990
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WPI; 1990-016567/03. P-PSDB; AAR04699.

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                                                            1274 TGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCAGCTGCAGCTGTG
                                                                                                                                                   1334 AGCICTCCGGCTACGGCAAGCATGAGGCCTTGTTTCTATTCGGAGCGCCTGAAGG
                                                                                                                                                                                                         1394 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAA
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 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA
                                             ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCG
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1738..1780
/*tag= b
/note="synthetic 3' adaptor"
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                                                                                                                                                                                             It is modified in the patent by replacing one or more codons specifying a positively charged amino acid. The resulting analogues are inserted into a replicable expression vector which is used to transform or transfect a host cell which is grown to express a t-pA analogue. The t-pA analogue is useful for the treatment of diseases or disorders associated with the formation of thrombi in blood vessels e.g. infarctions, thrombosis and embolism. The analogue, in the 1-chain form, exhibits the properties of a proenzyme; however on plasmin-catalysed cleavage of the one-chain form, the activity of the 2-chain form is fully retained. Compared to native t-pA, it has a higher fibrin selectivity, this results in a fibrinolytic agent with a higher fibrin selectivity, as the fibringenolytic activity induced by the analogue is reduced (Updated on 25-MAR-2003 to correct PA field.)
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Pred. No. 4e-225;
0; Mismatches 5; Indels 0;
                                                                          New tissue plasminogen activator (t-PA) analogue -
with higher fibrin selectivity than native t-pa, useful for
treating infarction, thrombosis and embolism
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                                              cDNA sequence of native tPA gene is excised from plasmid pST112, digested with Banmiz and Salı to form plasmid pST118. (Updated on 03-0CT-2002 to add missing OS field.) (Updated on 25-WAR-2003 to correct PA field.)
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                                                                                                                                                        Sequence 2100 BP; 498 A; 595 C; 597 G; 410 T; 0 other;
                                                                                                                                                                                                 Query Match 94.4%; Score 1065; DB 10; Best Local Similarity 99.5%; Pred. No. 4.1e-225; Matches 1068; Conservative 0; Mismatches 5;
    Example 29; Fig 21; 68pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tPA with N-terminal peptide of plasminogen linked is more stable in vivo than the native form. It is useful as a thrombolygic agent in the treatment of vascular diseases eg myocardial infarction, pulmonary embolism etc.
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                            TGTACACAAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New tissue plasminogen activator - having N-terminal peptide of plasminogen linked to tissue plasminogen activator for increased stability in vivo.
                                                                                                                                                                                                                                                                                                                                              Plasmid pST112 encoding novel N-terminal for tissue plasminogen activator (tPA).
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94.4%; Score 1065; DB 11; Length 2100;
Best Local Similarity 99.5%; Pred. No. 4.1e-225;
Matches 1068; Conservative 0; Mismatches 5; Indels 0;
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                                                                                                                            935 GGCTGACGTGGGGGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGGCCTGAGGACAGTACA
                                                                                                                                                                                                                                                                                                                                                                1055 AGGCTGCCATCTTTGCCAAGCACACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1235 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1655 TGACTITGGGGCATCATCAGCTGGGGCCTGGGCTGTGGAAGAAGGATGTCCGGGTG
                                                            815 TAGGCAAGGTTTACACAGACACAGAGCCCCAGGCCACGGCACTGGGCCTGGGCCAAACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                               1115 TACTCATCAGCTCCTGCTGGATTCTCTGCCGCCCACTGCTTCCAGGAGAGATTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1295 ATGACATTGCGCTGCTGCTGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1355 TGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1016 TGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGGTG
                                                                                                                                                                                GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACACAGTACA
                                                                                                                                                                                                                                                               GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC
                                                                                                                                                                                                                                                                                                                                             416 AGGCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                        476 TACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   596 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCCAGGAGCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTTCTTTTCTATTCGGAGCGCGCTGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCCAGGCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076 TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1715 TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                  Intron, recombination; combinatorial gene; trans-splicing; gene therapy; polymerase chain reaction; PCR; primer; amplification; tissue plasminogen activator; tPA; plasmid TPA-KS+; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA clone of human tissue plasminogen activator (tPA) was amplified by PCR using the primers given in AAQ87368-69. The amplified tPA DNA (AAQ8730) was ligated into vector KS+ to obtain plasmid TPA-KS+. The construct was used in combinatorial methods involving RNA splicing-mediated shuffling of tPA domains, in plasmid piNU1 (AAQ87347) to generate novel tPAs having improved thrombolytic properties.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                       *tag= a
note= "signal sequence and finger-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New intron-mediated recombinant techniques - used for the generation and selection of novel genes and gene prods. for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2162 BP; 520 A; 606 C; 619 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1065; DB 16;
Pred. No. 4.1e-225;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/product= Kringle-1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= catalytic domain
                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/product= EGF-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 59-60; 87pp; English
                                                                                                                                                                                                                                                                           Location/Qualifiers
82..334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.5%;
Matches 1068; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US10146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              715..972
/*tag= d
/product= P
                                     (updated)
(first entry)
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                                                                                               Human tPA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9507351-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1993;
                                     25-MAR-2003
19-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1995,
                                                                                                                                                                                                                                                                                              sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in therapy
                                                                                                                                                                                                                                        Synthetic
AAQ87370;
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The present sequence represents the human tissue plasminogen activator gene. It was used to construct plamsid TPA-KS+, which is used in the course of the invention. The specification describes a purified course of the invention. The specification describes a purified sequence of a group II intron, including an exon binding site not naturally present in the intron and a second segment comprising a site acceptor, and a nucleophilic group for transesterifying a phosphodiester bond of an RNA. Together the two segments form an a phosphodiester bond of an RNA. Together the two segments form an phosphodiester bond of an RNA. Together the two segments form an a phosphodiester bond of an RNA. Together the two segments form an the first segment into substrate RNA by a reverse splicing reaction. The reverse-splicing introns are used, by specific cleavage and ligation of discontinuous nucleic acid, to generate new genes and gene products, of discontinuous nucleic acid, to generate new genes and gene products, manipulation, e.g. replacements for restriction enzymes) or immunologically active or signal-transducing proteins such as antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse splicing construct containing fragments of autocatalytic introns - able to cleave and ligate discontinuous nucleic acid for generating new genes and e.g. ribozymes, libraries of enzymes and
                                                  Plasmid pINVI; reverse-splicing intron; group II intron;
exon binding site; domain V motif; branch site acceptor;
nucleophilic group; trasserification; phosphodiester bond;
autocatalytic Y-branched intron; reverse splicing reaction; ds.
                                                                                                                                                                                                                                  'note= "signal sequence and finger-like domain"
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                  Human tissue plasminogen activator gene sequence.
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/*tag= b
/note= "BGF-like domain"
448..714
/*tag= c
/note= "Kringle-1 domain"
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/note= "Kringle-2 domain"
973..2162
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/note= "catalytic domain"
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                                                                                                                                                                          Location/Qualifiers
82..334
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815 TAGGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCCACTGGGCCTGGGCAAACATA
                                                                                                                                                                                   935 GGCTGACGTGGGAGTACTGTGATGTGCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA
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                                              GCACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
                                                                           TAGGCAAGGTTTACACACACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA
                                                                                                                                                                     ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACGGCA
                                                                                                                                                                                                                              GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACACAGTACA
                                                                                                                                                                                                                                                                                         GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGC
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Length 2162; Indels

Score 1065; DB 19; Pred. No. 4.1e-225; 0; Mismatches 5;

94.48;

Best Local Similarity 99.5 Matches 1068; Conservative

Query Match

0; Mismatches

26

CCCAGGCGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG 115

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patentors claim a novel recombinant human t-PA which is resistant to specific enzymatic cleavage because it is stabilised by site-directed mutagenesis at a 2-chain cleavage site. Partic: the natural Arg at position 275 is replaced by Gly or Glu, or Ile at position 276 is replaced by Gly or Glu, or Ile at position 276 is replaced not 276 refer to the posn. of the AAS in the mature protein; i.e. AAS 310 and 311 of AAP60790). Also new are (1) DNA sequences; (2) expression vectors; and (3) microorganisms and cell cultures transformed with these vectors.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA
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                                                                                                                    (pre-t-PA)
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                                                                                                                Sequence encoding human pre-tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2547 BP; 627 A; 688 C; 691 G; 541 T; 0 other;
                                                                                                                                            Plasminogen conversion; vascular disease therapy;
                                                                                                                                                                                                  Location/Qualifiers
87..191
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              AAN60659 standard; DNA; 2547
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85US-0725468.
86US-0846697.
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P-PSDB; AAP60790.
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Matches 1068; Conserv
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22-APR-1985;
01-APR-1986;
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135 TACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGGTTTCCGC 1194
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                                              CCCACCACTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGG
                                                                                                                                                AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA
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/note= "from immunoglobulin kappa light chain gene"
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/label= TPA cDNA
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/note= "as above"
2165..4463
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07-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence was obtained from cDNA prepd. from mRNA extracted from-bowes melanoma cells. The cDNA was used to construct a gene library which was screened with a partial t-PA cDNA clone. Plasmid pKG12 was isolated and shown to comprise the whole coding region for human t-PA as well as 10.2bp 5'flanking, 760 bp 3' flanking DNA and a poly A tail. See also AAN91608. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified tissue plasminogen-activator - having domains deleted and amino acid changes to increase biological half-life and reduce inactivation.
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94.4%; Score 1065; DB 10; Length 2560;
Best Local Similarity 99.5%; Pred. No. 4.2e-225;
Matches 1068; Conservative 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2560 BP; 634 A; 690 C; 689 G; 547 T; 0 other;
                                              Location/Qualifiers
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/product=t-PA
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P-PSDB; AAP93716.
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  sapiens
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                                                                     sig_peptide
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  Ношо
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Vector pEMp1-tpa is an example of a vector of the invention. Pref.

the blocking element is a promoter sequence oriented with its native

s end disposed proximal to the enhancer element and its 5' end
disposed blocking element comprises a promoter sequence with its 5'
end disposed proximal to the enhancer element and, at its 3' end, a
gene encoding for a different protein of interest, (see FT). The
vector pEMp1 was constructed by inserting an enhancer-blocking
element into pEM1.

The CDNA fragment was inserted into the unique KhoI site present in
both pEM1 and pEMp1. Of 26 transformants obtd. with pEM1-tpa, 5
produced TPA at levels of 140-500 IU/m1. Of 16 transformants obtd.

C Updated on 31-CT-2002 to add missing OS field.)

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                       chain (IgH)"
                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA construct for high level expression of protein - having blocking element so that marker protein is produced only at levels required for selection
                       /note= "contg. the ampicillinase gene and bacterial origin of replication" complement (4464..6436)
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                                                                                                                                                                                                                                  blocking element'
                                                                                                                                                                         '*tag= i
'label= SV40 enhancer (TZ bp repeat)
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                                                                                                                                                                                                                                                        *tag= k
note= "from immunoglobulin heavy
                                                                                                                                                                                                                                                                                                          /note= "from metallothionine 17467..7533
                                                                                                /*tag= g
/label= SV40 origin region
                                                                       .coli gpt gene
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/label= SV40 (gpt) CAP
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/label= lambda-1
/note= "functions a
6972..7281
'*tag= e
'label= pBR322
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/label= MT (
1930..1935
/*tag= n
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'label= E.o
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(ABBO ) ABBOTT
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                                                                                                                       misc_signal
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                                                                                                                                                                                                                                                                                   promoter
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94.4%; Score 1065; DB 8; Length 7533; 99.5%; Pred. No. 4.8e-225;

Best Local Similarity

Query Match

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1052
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                                                                                              GCACGCACAGCCCCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
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                                                                                                                                       TAGGCAAGGTTTACACACACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA
                                                                                                                                                      TAGGCAAGGTTTACACAGGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA
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                          CCCAGGCGGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG
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/label=pBR322
/note="contg. ampicillinase gene and origin of
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4464..6971
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|labe|=K_3'UT
|note="from Ig kappa light chain gene"
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note="kappa 3 flanking sequence"
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note="from lambda promoter"
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|abel=pSV2-gpt
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note="from_SV40(gpt)"
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/note="from $V40"
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'note="lambda mRNA"
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/label=tPA_cDNA
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The plasmid was prepd by cleaving the very long 3' UT of t-PA cDNA (which causes mRNA instability) 34 nucleotides downstream of stop codon and inserting it into a pEMp1 vector. The pEMp1 vector was constructed from the following components (see feature table):

(a) a 2.25 PvuII-BamHI fragment from pSV2-gpt contg. the SV40 enhancer and early region promoter, the E.coli gpt gene, the SV40 small tumour antigen intervening sequence, and the SV40 termination and polyadenylation signals;

(b) a 2.3 kb PvuII-ECORI fragment from pBR322 contg. the ampicillinase gene and the bacterial origin of replication;

(c) a 0.3 kb PvuII-ECORI fragment contg. an Ig heavy chain enhancer;

(d) a 0.25 kb SacI-BQ1II fragment from the 3' UT of Ig kappa light chain gene; and

(f) a 0.26 kb xbaI-batNI fragment contg. the Ig light chain promoter,

(f) a 0.26 kb xbaI-batNI fragment contg. the Ig light chain promoter,

The expression plasmid can be used to transform host cells esp.
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                                 /*tag= q
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                                                                                                                                                                                                                                                                                                                                                                      Hybrid plasminogen activator comprises human tPA activator and N-terminal crosslinking domain from alpha2-plasmin inhibitor useful to treat thrombosis and image blood clots
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TYPE: nucleic acid
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 58, Appli Sequence 3, Appli Sequence 60, Appli Patent No. 5185259 Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Patent No. 5244676 Sequence 40, Appl Patent No. 5200340 Sequence 12, Appl Sequence 122, Appl	OR & NEUSTADT, TE 400	
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9920 9911.0 9911.0 9911.0 9911.0 9911.0 9911.0 9911.0 9911.0 9911.0 9911.0 9911.0 9911.0 9911.0	DPJ MASS SPA SPA NO NO NO NO NO NO NO NO NO NO	TELEPHONE: 703-413-3000 TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1419 base pairs TYDE: miclei acid
1038 1035.4 1030 924 924 798 625.8 625.6 170.8 170.8 170.8	RESULT 1  US-08-811-949-62  Sequence 62, Applicat Patent No. 5840533 GENERAL INFORMATION: APPLICANT: SASAKI APPLICANT: SASAKI APPLICANT: SASAKI APPLICANT: SASKI APPLICANT: ROBAYA TITLE OF INVENTION: NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: DELC STREET: 1755 S. CITY: WA COUNTRY: USA ZIP: 22202 COMPUTER READBLE MEDIUM TYPE: FI COMPUTER READBLE MEDIUM TYPE: FI COMPUTER READBLE SOFTWARE: PALC CURRENT APPLICATION: ATTORNEY/AGENT INF PILING DATE: OF CLASSIFICATION: ATTORNEY/AGENT INF NAME: OBLON NUMB FILING DATE: OF CLASSIFICATION: REFERENCE/DOCCKET TELECOMMUNICATION TELECOMUNICATION TELECOMMUNICATION TELECOMUNICATION TELECOMUNICATION TELECOMUNICATION TELECOMUNICATION	TELEPHON TELEFAX: ORMATION EQUENCE C LENGTH:
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94.4%; Score 1065; DB 2; Length 1419;

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                                                                                                          Sequence 10, Application US/08814412
| Patent No. 6150141
| GENERAL INFORMATION:
| APPLICANT: Jarrell Ph.D., Kevin A. | TITLE OF INVENTION: Intron-Mediated Techniques and Reagents NUMBER OF SEQUENCES: 46
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1848;
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ilarity 99.5%; Pred. No. 8.6e-290;
Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPENATING SYSTEM: PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,412
FILING DATE: 11-MAR-1997
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: Jarrell Ph.D., Breenda H.
REFERENCE/DOCKET NUMBER: 39,223
REFISTRATION NUMBER: 39,223
REFISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 248 5000
TELEPHONE: 617 248 4000
INFORMATION FOR SEQ 1D NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                ADDRESSEE: Choate, Hall & Stewart
STREET: 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IMMEDIATE SOURCE:
; CLONE: amplified t-PA clone
US-08-814-412-10
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 1068; Conserv
                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: MA
COUNTRY: USA
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    7.7e-290;
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    99.58;
Best Local Similarity 99.5
Matches 1068; Conservative
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998 AGGTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCA 1057
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                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INPORMATION:

NAME:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

REJERENCE/DOCKET NUMBER:

TELERENCE/DOCKET NUMBER:

TELERENCE/TOOKET NUMBER:

TELERENCE
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     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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; LOCATION: 25..
US-08-811-949-42
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: HAYASHI, MASAKA
APPLICANT: HAYASHI, MASAKAU
APPLICANT: NOTANI, JOUJI
APPLICANT: OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPENDING ADRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARAINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Patent No. 5840533
GENERAL INFORMATION:
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Best Local Similarity 99.5%; Pred. No. 9.2e-290;
Matches 1068; Conservative 0; Mismatches 5;
                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOGATION: 448.714
OTHER INFORMATION: /product= "Kringle-1 dor
FEATURE:
NAME/KEY: misc_feature
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                                          1298 TGGTCCGCACTGTGCCTTCCCCCGGCGACCTGCAGCTGCCGGACTGCG
                                                                                                                                                            TGGTCCGCACTGTGTCCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTG
                                                                                                                        776 AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGG
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Patent No. 549851

GENERAL INPORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
MUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 82..334
OTHER INFORMATION: /product= "Signal Sequence and
OTHER INFORMATION: Finger-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: OC109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,512
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELEFRAX: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEGUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
"WURD: murcleic acid
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STRANDEDNESS: doub
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                                                                                                                                                                                                                      Length 2162;
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OTHER INFORMATION: /product= "Kringle-1 domain"
NAME/KE:
NAME/KE: misc_feature
LOCATION: 715..972
OTHER INFORMATION: /product= "Kringle-2 domain"
                                                                                                                      Query Match
94.4%; Score 1065; DB 1;
Best Local Similarity 99.5%; Pred. No. 9.2e-290;
Matches 1068; Conservative 0; Mismatches 5;
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                                                              1475 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAA 1534
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                                                                                                                            1535 CAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGGGGGCCCCAGGCAAACT
                           AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTTAACAGAA
                                                                                                     CAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACT
                                                                                                                                                                                  TGCACGACGCCTGCCAGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA
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                                                                                                                                                                                                                                                                                                                                                 TGTACACAAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Jarrell, Kevin A.
TITLE OF INVENTION: AND REAGENTS
TITLE OF INVENTION: AND REAGENTS
CORRESPONDENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

LOCATION: 82.334

LOCATION: 82.334

Patent NFORMATION: /product= "Signal Sequence and Datent NFORMATION: Finger-like domain"

FRAUTHS: NAME/KEY: misc_feature

LOCATION: 335..47

CTHER INFORMATION: /product= "EGF-like domain"

FRAUTHS: NAME/KEY: misc_feature

LOCATION: 448..714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,0158
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HUV-008.02
TELEGRAM: (617) 832-1000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LIGE DAME: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08488015B Patent No. 5780272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-488-015B-3
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     875 ATTACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGCTGAGAAGAACCGCA 934
                                                                                                                                                                                                                            995 GCCAGCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1115 TACTCATCAGCTCCTGCTGGATTCTCTGCCGCCCACTGCTTCCAGGAGAGAGTTTCCGC
                                                             GGCTGACGTGGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCCTGAGACAGTACA
                                                                                                                 935 GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA
                                                                                                                                                                        GCCAGCCTCAGTTTCGCATCAAAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               596 AGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        656 ATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCG
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Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: MOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANIS, SEQUENCES:
CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
APPLICANT: Jarrell, Kevin A.
TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
TITLE OF INVENTION: AND REAGENTS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
ZIP: D2109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: C-DOS/MS-DOS
SOFTWARE: ASCII (text)
COMPUTER: ASCII (text)
SOFTWARE: ASCII (text)
COMPUTER: ASCII (te
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Pred. No. 9.2e-290;
0; Mismatches 5;
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REGISTRATION NUMBER: 36,709
REPERENCE/DOCKET NUMBER: HUV-008.02
TELECHONE: (617) 832-1000
TELEPHONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
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Best Local Similarity 99.5
Matches 1068; Conservative
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MOLECULE TYPE: CDNA
US-08-488-0158-25
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1019 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAA 1078
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     719 CCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGC 778
                                                            AGCICICCGGCTACGGCAAGCATGAAGGCCTTGTCTTTCTATTCGGAGCGCTGAAGG
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Pred. No. 2.4e-289;
0; Mismatches 6;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
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Best Local Similarity 99.4%;
Matches 1067; Conservative
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                       STREET: 1755 S. JEFFERSON DAVIS HIGHTON.
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION NUMBER: 24,618
RECISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/OCKET NUMBER: 18-966-0
TELEPHONE: 703-413-220
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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; LOCATION:
US-08-811-949-48
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1064 AGGCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCA 1123
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9
                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 7841-062
REFERENCE/DOCKET NUMBER: 7841-062
REFERENCE/DOCKET NUMBER: 7841-062
REFERENCE/JOCKET NUMBER: 7841-062
REJERGATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                     COMPUTER: Flopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-08-883-795A-39
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ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ORIGINAL SOURCE:
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                                                                                GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGC
                                                                                                                       GCCAGCCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGC
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APPLICANT: Delcuve, Genevieve
APPLICANT: Delcuve, Genevieve
APPLICANT: Delcuve, Genevieve
APPLICANT: Delcuve, Genevieve
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: APCORTO
STATE: Ontario
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US-08-883-795A-39.
Sequence 39, Application US/08883795A
; Patent No. 5985607
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1287 TGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCCGGACTGGACGGAGTGTG 1346
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Fatent No. 5561053
GENERAL INFORMATION:
APPLICANT: Crowley, Craig W.
TITLE OF INVENTION: METHOD FOR SELECT:
TITLE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
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US-08-286-740-1
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1364 TGGTCCGCACTGTGTGCCTTCCCCCGGCGACCTGCAGCTGCCGGACTGGACGGAGTGTG
                                                                                                                                  1484 AGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATTCATATACTTAACAGAA
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94.3%; Score 1063.4; DB 6; Length 2457;
Best Local Similarity 99.4%; Pred. No. 2.7e-289;
Matches 1067; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S344773-1
;Patent No. 5344773
;Patent No. 5344773
;APPLICANT WEI, CHA-MER;HSIUNG, NANCY;REDDY, VERMURI B.;
;LEMONTT, JEFFERY F.;DACKGWSKI, WILLIAM;DOUGLAS, RICHARD;
;COLE, EDWARD S.;PURCELL JR., RICHARD D.;LAU, DAVID TAI-YUI
;TITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN
;ATIVATOR PRODUCED BY RECOMBIANT DNA
;ATIVATOR PRODUCED BY RECOMBIANT DNA
;ATIVATOR PRODUCES: 6
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/782,686
;FILING DATE: 01-OCT-1985
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 656,770
;FILING DATE: 01-OCT-1984
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                                                                 2835 ATGACATTGCGCTGCTGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGGC 2894
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; GENERAL INFORMATION:
APPLICANT; GENERITECH, INC.
ITILE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
ITILE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09576
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286740
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 798PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STRANDEDNESS: double
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PCT-US95-09576-1
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PCT-US95-09576-1
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WEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,740
FILING DATE: 05-AUG-1994
CLASSIFICATION SATA:
APPLICATION UMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION TOWNER: TELECOMMUNICATION TOWNER: SEQUENCE CHARACTERISTICS: LENGTH: 7360 bases

LENGTH: 7360 bases
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STRANDEDNESS: double
TOPOLOGY: linear
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1076 TGTACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
                                                                                               Sequence 44, Application US/08811949; Patent No. 5840533; GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: double
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               Length
                                         6; Indels
             DB 5;
             Score 1063.4; DB 5
Pred. No. 4.3e-289;
0; Mismatches 6;
          Query Match
Best Local Similarity 99.4%;
Matches 1067; Conservative
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Length 1068;
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ADDRESSEE: P.C.
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MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Date of the compatible
COMPUTER: Date of the compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: OS-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-2220
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
TEMETAL: 1068 base pairs
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                                                                                                                                                                                                                                APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASATI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HOTANI, JOUJI
APPLICANT: KOBAYASHI, MASKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
WINMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.0%; Pred. No. 4.8e-289;
Matches 1062; Conservative 0; Mismatches 0;
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                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON NORMAN F.
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                               JEFFERSON DAVIS HIGHWAY, SUITE 400
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Pred. No. 6e-289;
0; Mismatches 7;
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Best Local Similarity 99.3%;
Matches 1066; Conservative
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TELEPAX: 703-413-220
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
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STRANDEDNESS: double
STREET: 1755 S. J. CITY: ARLINGTON STATE: VA COUNTRY: USA ZID.
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US-08-811-949-50
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                               TITCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCTGGCAGGCTGCCATC
                                                                                                                                                                                         TTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGC
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APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASHI, YOSHIMASA
APPLICANT: SASHI, MASAK,
APPLICANT: NOTANI, JOULI
APPLICANT: NOTANI, JOULI
APPLICANT: NOTANI, MASAKAU
APPLICANT: NOTANI, MASAKAU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
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US-08-811-949-50
; Sequence 50, Application US/08811949
; Patent No. 5840531
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MOLECULE TYPE: DNA (genomic)
FEATURE:
                  TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1974 base pairs
   703-413-3000
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STRANDEDNESS: double
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
STATE: VA
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-WAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/08811949
Patent No. 5840533
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US-08-811-949-38
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896 CAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGGGGGG	1351 CAGTCACCGACAAGATGCTGTGTGTGTGTGTGTGTGTGTG	956 TGCACGCCTGCCAGGCCGATTCGGGAGGCCCCTGGTGTCTGAACGATGGCCGCA 1015	1411 TGCACGACGCCTGCCAGGGCGATTCGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCA 1470	1016 TGACTTTGGTGGGCATCATCATCAGCTGGGCTGGGGCTGGACAGAAGGATGTCCCGGGTG 1075	1471 TGACTTTGGTGGGCATCATCAGCTGGGCCTGTGGACAGAAGGATGTCCCGGGTG 1530	1076 TGTACACAAAGGTTACCAACTACCTAGATTCGTGACACACATGCGACG 1128	1531 TGTACACAAAGGTTACCAACTACCTAGACTGCGATCGTGACAACATGCGACCG 1583	Search completed: August 19, 2003, 08:35:06 Job time : 90.2804 secs
ò	qa	È	a a	ò	g	ò	qq	Search Job ti

us-09-987-455-2.rnpb

- nucleic search, using sw model OM nucleic

August 19, 2003, 04:46:44; Search time 318.307 Seconds (without alignments) 7930.701 Million cell updates/sec Run on:

US-09-987-455-2 1128 Title: Perfect score:

1 atgaaaaagacagctatcgc.....ttcgtgacaacatgcgaccg 1128 Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

1504479 seqs, 1118970152 residues Searched:

Total number of hits satisfying chosen parameters:

3008958

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Published Applications NA:\*

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15: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
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17: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
18: /cgn2 /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query	Query Match Length DR TD	ä	Ē	Description
	1 0 0			}		
٦	1128	100.0	1128	11	US-09-987-455-2	Sequence 2, Appli
7	1128	100.0	1128	11	US-09-987-455-5	Sequence 5, Appli
٣	1063.4		1689	σ	US-09-969-271-6	Sequence 6, Appli
4	1063.4		2509	14	US-10-193-656-7	Sequence 7, Appli
S	1063.4		2519	6	US-09-969-271-5	Sequence 5, Appli
9	1062		1065	11	US-09-987-455-4	Sequence 4, Appli
7	1062	94.1	1065	1	US-09-987-455-7	Sequence 7, Appli
œ	1061.8		2641	10	US-09-974-298-144	Sequence 144, App
0	227.2		329	12	US-10-007-926A-433	Sequence 433, App
10	191.6		1212	10	US-09-880-503-15	Sequence 15, Appl
11	188		1415	14	US-10-198-846-12748	Sequence 12748, A
12	170.8		1475	6	US-09-735-705-122	Sequence 122, App
13	170.8		1475	10	US-09-850-716A-122	Sequence 122, App
14	170.8		1475	10	US-09-897-778-122	Sequence 122, App
15	170.8		1475	1	US-09-466-396A-122	Sequence 122, App
16	170.8		1475	12	US-10-117-982-122	Sequence 122, App

61 GCGGCCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACG 120

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Sequence 159, App Sequence 46, Appl Sequence 1, Appl Sequence 123, App Sequence 160, App Sequence 160, App Sequence 160, App Sequence 1689, App Sequence 1689, App Sequence 1689, App Sequence 1689, App Sequence 1689, App Sequence 1689, App Sequence 164, Appl Sequence 164, Appl	sequence 1512, App Sequence 1613, Ap Sequence 18438, A Sequence 237, App Sequence 237, App Sequence 12715, A Sequence 35, App
US-10-101-510-159 US-09-971-39-46 US-10-076-421-1 US-09-735-705-123 US-09-850-776A-123 US-09-86-1776A-123 US-09-466-396A-123 US-10-117-982-123 US-10-117-982-123 US-10-117-982-123 US-10-117-982-123 US-10-117-982-123 US-10-117-982-160 US-10-131-183 US-09-864-761-1683 US-09-880-503-14 US-09-880-503-14 US-09-980-503-14 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16 US-09-980-503-16	US-09-594-4505-552 US-09-864-761-18438 US-09-918-955-11188 US-09-920-300A-237 US-10-033-528-237 US-09-918-995-12715 US-09-918-995-12715
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## ALIGNMENTS

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APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: MAD-Derived tpA or K2S Molecules
FILE REFERENCE: 0552.219001
FILE REFERENCE: 0552.219001
GURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 06/268,574
PRIOR PLILING DATE: 2001-215
PRIOR PLILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: coding; OTHER INFORMATION: sequence for OmpA-K2S fusion protein US-09-987-455-2
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100.0%; Pred. No. 0;
ive 0; Mismatches
                      Sequence 2, Application US/09987455 Publication No. US20030049729A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 1128
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Matches 1128; Conservative
US-09-987-455-2
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CACAGCCTCGAGGGAAACGGCTCCTCTCTCTCTCGGGATGGGTCAGGCTCAGGCTCAGGGATGGGTCAGGCTCAGGCTCAGGGTCAGGGAAACGGTCAGGGTCGGGAACTGCTCTCTCT	1	; Sequence 5, Application US/09987455 ; Publication No. US20030049729A1	; GENERAL INFORMATION: ; APPLICANT: Aranya Manosroi ; APPLICANT: Jiradej Manosroi	ات - بوبر بروبر	or K2S	; CURRENT APPLICATION NUMBER: US/09/987,455 ; CURRENT FILING DATE: 2001-11-14 ; DPIOD ADDITORION NUMBED: 67/368 674	PRIOR FILING DATE: 2001-02-15 ; PRIOR APPLICATION NUMBER: GB 0027779.8 ; PRIOR FILING DATE: 2000-11-14	; NUMBER OF SEQ ID NOS: 25 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 5 ; LENCHH: 1128	; TYPE: DNA ; ORGANISM: Artificial Sequence ; FRATURE:	; OTHER INFORMATION: Description of Artificial Sequence : OTHER INFORMATION: sequence for OmpA-K2S fusion prote	US-09-987-455-5 Query Match 100.0%; Score 1128; DB 11;	Best Local S Matches 1128	Oy 1 ATGAAAAGACTGCTATCGCGATTGCAGTGGCTGGTTGTTTTTTTT	Qy 61 GOGGCCTCTGAGGGAAACAGTGCTACTTTGGGAATGGG	61	0y 121 CACAGCCTCACGAGTGGGGTGCCTCCTGCCGTGGAATT	181	Db 181 AAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGC	QY. 241 TGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTG DY. 241 TGCCGAAATCCTGATGGGAATGCCAAGCCTGATGTG DA 241 TGCCGAAATCCTGAAGCGAAGCCTAAGAGCCTAAGAGCAAGAGCAAGAGCAAGAGAAGAAGAAGAAGAAGAA	301	Db 301 ACGIGGGAGTACTGTGATGTGCCCTCCTGCTGCGGC	361 C	361 C	Oy 421 GCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCCGTTTC	421		Qy 541 CACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCTTC
		I GUGGLUTUTGAGGGAAAUAGTGAUTGUTAUTTTGGGAATGGGTCAGUUTGGCAUG	1 CACAGCCTCACCAGTCGGGTGCCTCCTGCCTCGGAATTCCATGATCGATAGGC	AAGGTTTACACAGACACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTAC	TGCCGGAATCCTGATGGCGGATGCCAGGTGCCAGGTGCTGAAGAACCGCAGGCTG		ACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACTGGGGCCTGAGACAGTACAGCCGG	61 CCTCAGTTTCGCATCAAAGGAGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCT	GCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGGTTACTC	<ul> <li>GCCATCTTTGCCAAGGCACAGGAGGCCGGAGCGGTTCCTGTGCGGGGGCATACTC</li> </ul>	81 ATCAGCTCCTGCTGGATTCTCTGCCGCCACTGCTTCCAGGAGAGGTTTCCGCCCCACTGCTTTCCAGCACGTTTCCGCCCCACTGCTTTCCAGCACGTTTCCGCCCCACTGCTTTCCAGCACGTTTCCGCCCCACTGCTTTCCAGCAGAGAGATTTCCGCCCCACTGCTTTCCAGCAGAGAGATTTCCGCCCCACTGCTTTCCAGCAGAGAGATTTCCGCCCCACTGCTTTCCAGCAGAGAGATTTCCGCCCCACTGCTTTCCAGCAGAAGAGATTTCCGCCCCACTACTTTCCAGCAGAAGAGATTTCCGCCCCACTACTACACACAC	CACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGAAAAAAAA	CACCTGACGGGGATCTTGGGGCAGAACATACCGGGTGGTCCCTGGGGGGGG		ATTGCGCTGCTGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTC	ATTECHETISCHEGAGETGAAATTEGFECCGGCTGTGCCCAGGAGGGGGGGGTGCCCGGCGGGCCGGGGCGGGGCGCGGCCCGGGAGGTGCAGCTGCCGGAGCTGCCGGAGCTGCCGGAGCTGCCGGAACTGCAGCTGCCGGAACTGCAGCTGCCGGAACTGCAGCTGCCGGAACTGCAGCTGCCGGAACTGCAGCTGCCGGAACTGCAGCTGCCGGAACTGCAGCTGCCGGAACTGCAGCTGCAGCTGCCGGAACTGCAGAACTGCAGAACTGCAGAACTGCAGAACTGCAGAACTGCAGAACTGCAGAACTGCAGAAACTAGAACAACAAAAAAAA		TCCGGCTACGGCAAGCATGAGGCCTTGTCTTCTATTCGAAGGGGGTGAAGGAGGCT	1 TCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGGGGCTGAAGGGTT CATGTCAGACTGTACCCATCCAGCGCGCTGCACAATCAAACAATTAACTTAACAATTAACAAACA		ACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGCCCCAGGCAACTTGCAC	accgacaacatgctgtgtgctggagacacacgggcggggcgggc	GAGGCCTGCCAGGCGATTCGGGAGGCCCCCTGGTGTCTGAACGATGGCCGCATGACT	LACIGUCIGUE AGGAGUGATITUGAGAGGUCUCU TGAGTGTUTUCUGAACGATGGCCGCATGACT     THE CHARLOCATA AGGAGGAGGUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCU	TIGGT/GGG/ATCATCAGC/GGGGC/TGGGGCT/GTGGAAAGGATGT/CCCGGGTGT/GTACAGAAGGATGT/CCCGGGTGT/GTACAGAAGGATGT/CCCGGGGTGT/GTACAGAAGGATGT/CCCGGGGTGT/GTACAGAAGGATGT/CCCGGGGTTGT/GTACAGAAGGATGT/CCCGGGGTTGTGTACAGAAGGATGTTCACAGAGGAATGT/CACAGAGTGTACAGAAGGATGTTGTACAGAGAAGGATGTTGTACAGAGAGGATGTTGTACAGAGGATGTTGTACAGAGGATGTTGTACAGAGGATGTTGTACAGAGGATGTTGTACAGAGGATGTTGTACAGAGGATGTTGTACAGAGGATGTTGTACAGAGGATGTTGTACAGAGAGAG	1 ACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128	1081 ACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128

ô GCTCAGCCTACCGTGGCACG 120 CCTGTGCGGGGGCATACTC 480 GGAGAGGTTTCCGCCCCAC 540 TTCCATGATCCTGATAGGC 180 CCTGGGCAACATAATTAC 240 CCTGAGACAGTACAGCCAG 360 CCTCCCACCCCTGGCAGGCT 420 TTTCGCTACCGTGGCCCAG 60 0; Gaps ion of Recombinant as Length 1128; nce: coding otein Indels 엄

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                                                                                 GCCTGACGTGGGAGTACTGTGTGTGCCCTCCTCCTCCACCTGCGGCCTGAGACAGTACA
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                                                                  GGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACA
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APPLICANT: HOLMDAHL, Rikard
APPLICANT: LI, Jinan
TITLE OF INVENTION: NOVEL DRUG TARGETS FOR
FILE REFERENCE: 3810/10577-US3
CURRENT APPLICATION NUMBER: US/10/193,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10193656; Publication No. US20030096733A1; GENERAL INFORMATION:
APPLICANT: NOT TOT APPLICANT: LI, Jinan APPLICANT: LI, Jinan ; TITLE OF INVENTION: NOVEL DRUG TARGET; FILE REFERENCE: 3810/10577-US3;
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US-10-193-656-7
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Patent No. US20020098179A1

GENERAL INFORMATION:

APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));

APPLICANT: Pfizer Limited (GB and EP (GB) only);

TITLE OF INVENTION: Pharmaceutical Combinations

FILE REFERENCE: PCS.10951APME

CURRENT APPLICATION NUMBER: US/09/969,271

PRIOR PILING DATE: 2001-10-01

PRIOR PILING DATE: 2001-10-01

PRIOR FILING DATE: 2001-10-01

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: PastSEQ for Windows Version 4.0
                                                    CATGTCAGACTGTACCCATCCAGCCGCTGCACACACATTACTTAACAAAAACAGTC
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                TTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGAC
                                                                                                        CGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACTGTGAGCTC
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Pred. No. 0;
0; Mismatches
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larity 99.4%;
Conservative
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Best Local Simil
Matches 1067; C
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| Patent No. US20020098179A1
| GENERAL INFORMATION:
| APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB)
| APPLICANT: Pfizer Limited (GB and EP (GB) only)
| TITLE OF INVENTION: Pharmaceutical Combinations
| FILE REFERENCE: PCS10951APWE
| CURRENT APPLICATION NUMBER: US/09/969,271
| PRIOR APPLICATION NUMBER: GB 0025473.0
| PRIOR FILING DATE: 2000-10-17
| NUMBER OF SEC 10 NOS: 7
| SOFTWARE: PastSEQ for Windows Version 4.0
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99.4%; Pred. No. 0;
live 0; Mismatches
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DATRABASB CECESSION NUMBER: Genbank / X07393
DATRABASE ENTRY DATE: 1995-03-27
RELEVANT RESIDUES: (1)..(2509)
          PRIOR APPLICATION NUMBER: US 60/304,461
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 2509
2002-07-10
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.4 Matches 1067; Conservative
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   FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: sequence for K2S protein
                                                                         Query Match
94.1%; Score 1062; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches
    ; FEATURE:
; OTHER INFORM;
; OTHER INFORM!
US-09-987-455-4
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Publication No. US2003004972941

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Jiradej Manosroi

APPLICANT: Chatchai Tayapiwatana

FILE OF INVENTION: Methods for Large Scale Production of Recombinant

TITLE OF INVENTION: Methods for Large Scale Production

FILE OF INVENTION: Methods for Large Scale Production

CURRENT APPLICATION NUMBER: US/09/987,455

CURRENT APPLICATION NUMBER: 60/269,574

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-02-15

PRIOR FILING DATE: 2001-11-14

NUMBER: OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 1065

TYPE: DNA

CREANISM: Artificial Sequence
                                                                                                   AGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTTTCTATTCGGAGCGGCTGAAGG
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                                                             110 TACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGC
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TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGGGTTTCCGGCCCCACCACCTG 480
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                                    547 ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAA
                                                                                                                                                                                                                         CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCCAGGAGAGCAGCGTGGTCCGCACT
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CB1
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Patent No. US20020156263A1

GENERAL INFORMATION:

APPLICANT: Chen, Huel-Mei

TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER

FILE REPERBUCE: PA-0037 P

CURRENT APPLICATION NUMBER: US/09/974,298

CURRENT FILING DATE: 2001-10-04

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 194

SEQ ID NO 144

LENGTH: 2641
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94.1%; Score 1061.8;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1066; Conservative 0; Mismatches
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; LOCATION: 2635
; OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-144
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Chacchai Tyapiwatana
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.190001
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
                     961 GGCATCATCAGCTGGGCCTGGGCCTGTGGAAGGAAGGATGTCCCGGGTGTGTACACAAAG
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                                                                       GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1128
                                                                                          GITACCAACTACCTAGACTGGATTCGTGACAACATGCGACCG 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.1%; Score 1062; DB 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 0;
                                                                                                                                                                                                   Sequence 7, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
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                                                                                                                                                                 RESULT 7
US-09-987-455-7
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sequence. Homo sapiens plasminogen activator (PLAT)
                            Sequence 433, Application US/10007926A

Sequence 433, Application US/10007926A

Publication No. US20030143539A1

GENERAL INFORMATION:

APPLICANT: BERTUCCI, FRANCOIS

APPLICANT: BIRNBAUM, DANIEL

APPLICANT: BIRNBAUM, DANIEL

APPLICANT: BIRNBAUM, DANIEL

APPLICANT: BIRNBAUM, DANIEL

APPLICANT: WINNER, CATHERINE

APPLICANT: WINNER, PATRICE

TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

FILE REFERENCE: 1546-R-00

CURRENT FILNG DATE: 2001-12-07

PRIOR FILING DATE: 2001-12-07

PRIOR FILING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 468

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 433
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Pred. No. 5.9e-62;
0; Mismatches 6; Indels
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; OTHER INFORMATION: a, t, c or
US-10-007-926A-433
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Best Local Similarity 97.4%;
Matches 229; Conservative
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CCATION: (57)
COTHER INFORMATION: a, t, c
FEATURE:
NAME/KEY: modified_base
LOCATION: (82)
OTHER INFORMATION: a, t, c
FEATURE:
MAME/KEY: modified_base
LOCATION: (182)
COTHER INFORMATION: a, t, c
FEATURE:
CCATION: (159)
OTHER INFORMATION: a, t, c
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NAME/KEY: modified_base
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OTHER INFORMATION: a,
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US-09-880-503-15
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                        810 CCCCTGCCTGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTG
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                                                                            GCACGCACACCCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGA
                                                                                                                                                         176 TAGGCAAGGTTTACACACACACACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATA
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LOCATION: 1, 2, 3, 1414, 1415
OTHER INFORMATION: n = A,T,C or G
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Matches 255; Conserv
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                        APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REPERENCE: 5956-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Petentin Ver. 2.1
SEQ ID NO 15
LENGTH: 1212
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TGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCAC
                                                              924 TGTGAAGCTGATTTCCCACCGGGAGTGTCAGCAGCCCCACTACTACGGCTCTGAAGTCAC
                                                                                                                                    CGACAACATGCTGTGTGCTGGACACTCGGAGCGGCGGGCCCCCAGGCAAACTTGCCACGA
                                                                                                                                                                                                             --AATGGAAAACAGA
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APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhao
APPLICANT: Wang, Youzhao
APPLICANT: Wang, Youzhao
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION WUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 2002-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FREESE FOR Windows Version 4.0
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1064 TCCGGAGCAGCTGAAGATGACTGTTGTGAAGCTGATTTCCCACCGGGAGTGTCAGCAGCC 1123
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                                                                                                                                                                                    CA-----CITACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               585 CGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGA
                                                                  824 GCAAGGGGAGATGAAGTTTGAGGTGGAAAACCTCCTACACAAGGACTACAGGGCTGA
                                                                                                                                                                                                                                                                                                                                                                     699 TGCCCAGGAGGAGCAGCGTGCTCCCCTGTGTGCCTTCCCCCCGGCGGACCTGCAGCTGCC
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Fatent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TILLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; TILLE REFERENCE: 210121.455C115
CURRENT APPLICATION WUMBER: US/09/850,716A
CURRENT FILLNG DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12.
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Pred. No. 9.6e-44;
0; Mismatches 457;
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51; Conservative C
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US-09-850-716A-122
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1132 CAGGCTGACGTGGGAGTACTGTGATGTGCCCTCTGTCACC 1171
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Moneill, Patricia D.
APPLICANT: Fanger, Neill.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; CURRENT APPLICATION UNMERS. US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12-2
                                                                                                                                                                                                                      Sequence 122, Application US/09735705
Patent No. US20020052329A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
Henderson, Robert A.
MCNeill, Patricia D.
Fanger, Neil
                                                                                                                                                                                                                                                                     | Patent No. US20020052329A1
| GENERAL INFORMATION:
| APPLICANT: Wang, Tongtong
| APPLICANT: Fan, Liqun
| APPLICANT: Ralos, Michael D.
| APPLICANT: Bangur, Chaitanya S.
| APPLICANT: Hosken, Nancy
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Best Local Similarity 51.3%;
Matches 551; Conservative 0
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; ORGANISM: Homo sapien
US-09-735-705-122
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APPLICANT: PECKERM, David W.
APPLICANT: PECKERM, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REPRENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT APPLICATION NUMBER: 2010-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 122
LENGTH: 1475
                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-09-897-778-122
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      DB 10; Length 1475;
                                         Indels
Score 170.8; DB 10;
Pred. No. 9.6e-44;
0; Mismatches .457;
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ilarity 51.3%;
Conservative 0
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Matches 551; Conserv
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Sequence 122, Application US/09897778 Patent No. US20020147143A1 GENERAL INFORMATION:

RESULT 14 US-09-897-778-122

APPLICANT: Wang, Tongtong
APPLICANT: Warnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro

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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REPERRENCE: 210121.45564
CURRENT APPLICATION NUMBER: US/09/466,396A
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 122, Application US/09466396A Publication No. US20030119763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 CTCCTGCTCCACCTGCGCCTGAG--
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Best Local Similarity 51.3%;
Matches 551; Conservative
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; ORGANISM: Homo sapien
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                                                                       GAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGG
                                                                                                                                                                                                                   CGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGGATGTCCCGGGTGTACACAAAGGTTACCAACTACCTAGACTGGATTCG
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Search completed: August 19, 2003, 14:22:22 Job time : 321.307 secs

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Scoring table:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM nucleic

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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4498.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOBAIO21ZDO8_C
S01980 laciluster=4498.r. Contact : Feng Liang Email :
Lilang@lifetech.com URL : http://fulllength.invitrogen.com/
InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX329047

BX329047 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA SATARA, MRNA SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 930)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                BU157720
BU257289
BI7652389
BI7652389
BE732704
BE732704
BE732413
BE732413
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BE732413
BU134603
BQ689840
BU179903
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BC899840
BU179903
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BU179903
BC8999940
BU15728
BC128855
CB128855
CB128855
CB12885
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442.8
41.1
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BX329047/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
BX329047 BX329047
BU149958 AGENCOURT
BX389609 BX389609
BU146167 AGENCOURT
                                                                                                                  August 18, 2003, 22:44:33 ; Search time 3299.95 Seconds (without alignments) 8307.845 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                               1 atgaaaaagacagctatcgc.....ttcgtgacaacatgcgaccg 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                       45562784
                version 5.1.6
- 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                  22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 summaries
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BU149958
BX389609
BU146167
                                                                                   - nucleic search, using sw model
                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 1.0
              GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
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99 best3: *
99 best3: *
99 best5: *
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em_gss_hum: *
em_gss_hum: *
em_gss_hum: *
em_gss_hum: *
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seq length: 200000000
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1128
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75.6
75.4
72.6
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EST 01-MAY-2003

Score

No. Result

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895 853 850.2 818.6

BQ699978 AGENCOURT BU15720 AGENCOURT BU15720 AGENCOURT BU15720 AGENCOURT BU157320 AGENCOURT BU157320 AGENCOURT BC15362 60273584 BC15362 60273584 BC15362 60273587 BC15362 AGENCOURT BC15721 AU134301 BC1687779 AGENCOURT BC1687779 AGENCOURT BC1689095 AGENCOURT BU179903 AGENCOURT BU157491 AGENCOURT BU157491 AGENCOURT BU157491 AGENCOURT BU15784 601308225 AU17846 AU13463 BE594944 601308225 AU17840525 K-EST0213 BC759384 601742678 BU157341 AGENCOURT CU158959 AGENCOURT CU1589412 AGENCOURT

29

8

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/ADDITION TO THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUL49958
AGENCOURT 8137213 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6184119 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 TGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGGAGTACTG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIST2 row: m column: 16
High quality sequence start: 18
High quality sequence stop: 644.
88 AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCCAGGCAAACTTGCACGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGAACCCCAGTGCCCAGGCACTGGGGCCTGGGGCAAACATAATTACTGCCGGAATCCTGA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 853; DB 13;
Pred. No. 2.5e-211;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6184119"
                                                                                                                                                                                                                                                                  TGCCAGGGCGATTCGGGAGGCCCCC 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           TGCCAGGCGATTCGGGAGGCCCCC
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BU149958
LOCUS
DEFINITION
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VERSION
KEYWORDS
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was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4498.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAF025ZG09_AF02376_3&cluster=4498.r.
Contact: Feng Liang Bmail: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAF025ZG09_AF02376_3.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
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AGENCOURT 7981262 Lupski dorsal root ganglion Homo sapiens cDNA
CODE IMAGE:6185661 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
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/dev stage="adult, 36 yr"
/lab_host="DH10B"
/clone=lib="Lupskt dorsal root ganglion"
/clone="Vector: pGWV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pGWV-SPORT6 (Life Technologies); Site_1:
/pite_1: sail; cDNM made by oligo-dT priming.
/pitectionally cloned using the following adaptors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
    Tissue Procurement: Dr. James R. Lupski
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
    DNA Sequencing by: Agencourt Bioocience Corporation
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
    Plate: LiAM1576 row: m column: 22
    High quality sequence stop: 665.
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:6185661"
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| organism="Memo sapiens" |
| organism="memo sapiens" |
| mol_type="mRNA" |
| db_xref="mRNA" |
| clone="mrAGE:6209120" |
| tissue_type="ductal carcinoma, cell line" |
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.
El (Bases I to 883)
NIH-MGC http://mgc.nci.nih.gov/.
In Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparati
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            360 CATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCCAGGAGAGCAGCGTGGT 419
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E 1 (bases 1 to 993)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCC
cnbA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
column: 10
High quality sequence stops: 681.
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Craniata, Vertebrata, Buteleostomi; Catarrhini; Hominidae; Homo.

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Mammalia; Butheria; Primates; Catarrhini; Hor
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished

sapiens (human)

Ношо

Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster.
4498.r. For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAF025ZG09\_AF02376\_Z&cluster=4498.r.
cgi-bin/cluster.cgi?seq=CSOBAF025ZG09\_AF02376\_Z&cluster=4498.r.
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAF025ZG09\_AF02376\_2.
Location/Qualifiers

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(Stratagene) and Superscript II RT (Life Technologies)
Note: this is a NIH MGC Library."
265 c 259 g 175 t
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                                                                                                              GGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAAT
                                                                                                                                        GGCAAGGTTTACACAGCACAGAACCCCCAGTGCCCAGGCACTGGGCCTTGGGCCAAACATAAT
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                                                           Score 811.2; DB 13
Pred. No. 1.9e-200;
0; Mismatches 8;
                                                            Query Match
Best Local Similarity 99.0%;
Matches 816; Conservative
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/organism="Homo sapiens"
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMYSPORT 6 vector. Library was normalized."
39 a 273 c 264 g 186 t 6 others
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                                                                                                                                                                                                                                                                                         DB 13; Length 918;
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                                                                                                                                                                                                                                                                                       71.6%; Score 807.6; DB 13
llarity 96.4%; Pred. No. 1.7e-199;
Conservative 0; Mismatches 29;
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Matches 855; Conserv
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EST 08-MAY-2003

BX389608

BX389608 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA COT 38-809608

BX389608.1 GI:30463469

DEFINITION

LOCUS

RESULT 7 BX389608

ACCESSION VERSION

us-09-987-455-2.rst

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KEYWORDS
SOURCE
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/tissue type="ductal carcinoma, cell line"
/lab.host="Ductal carcinoma, cell line"
/lab.host="Mill MGB (phage-resistant)"
/clone lib="MIH MGC 110"
/clone lib="MIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: Lihs is a NIH MGC Library."
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                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2316 row: e column: 21
High quality sequence stop: 630.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 888) NIH-WGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%; Score 782.8; DB 13; Length.
.larity 97.2%; Pred. No. 4.9e-193;
Conservative 0; Mismatches 17; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="blue" (phage-resistant)"
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E. (Dases 1 to 950)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lonpublished
Contact: Robert Strausberg, Ph.D.

Email: cgapba-rømail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CONA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The 1.MA.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the 1.MA.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2550 row: p column: 02
High quality sequence start: 35
High quality sequence start: 35
High quality sequence stop: 684.
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AGENCOURT 8775988 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6373489
5. mRNA Sequence.
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GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCCAGGAGAGCAGCGTG
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BQ927899.1 GI:22342930
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AUTHORS
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JOURNAL
COMMENT
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/Lone="Diagonal Color of the Co
                     Homo sapiens (Indumin)

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Rutheria; Butheria; Primates; Catarrhini; Hominidae; Homo.

Ruthoral Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://imagg-llnl.gov

Right quality sequence stop: 837.
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Pred. No. 3.1e-188;
0; Mismatches 1; Indels 1;
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Best Local Similarity 99.7%;
Matches 776; Conservative 0
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                                                                                                  Length 950;
                                                                                                                                                                                      CCACGTGCTGAAGAACCGCAGGCTGACGTGGGGAGTACTGTGATGTGCCC
                                                                                           ; Score 765.2; DB 13; Length; Pred. No. 2e-188; . 0; Mismatches 13; Indels
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NIH MGC Library."
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                                                                                       8 GAGGAACAGTGACTGCTATTATTGGGAATGGGACGGCCTACCGTGGCACAGCCACAGCCTCA
                                                                                                                                         CCGAGTCGGGTGCCTCCTCCC-GTGGAATTCCATGATCCTGATAGGCAAGGTTTAC
                                                                                                                                                                                                           ACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGGAAT
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                                                                     72 GGGAAACAGTGACTGCTACT-TTGGGAATGGGTCAGCCTACCGTGGCACGCACGCACGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 CGCATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTT
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     Length 948;
                                   Indels
     DB 10;
                                     52;
Score 706.8; DB 10
Pred. No. 3.2e-173;
); Mismatches 52;
                                   ő
 62.7%;
93.3%;
 Query Match 62.7
Best Local Similarity 93.3
Matches 793; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCIPENTY MIN MCC_39 Homo sapiens CDNA clone IMAGE:3611007 5', MRNA sequence.
                                                                                                                                                                                                        CGCATGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCG 1071
                                                                                                     540
                                                                                                                                                                         600
                                                                                                                                         951
                                                                                                                                                                                                                             891
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 948)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue types adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="WIH MGC 39"
/note="Organ aparcrass, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the Collowing 5' adaptor: GGCACGAR(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA syntheris kit (Stratagene) and Superscript II RT (Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contract: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Arror
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM267 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 759.
                   TGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCTTTCTATTCGGAGCGGCTG
                                                                                    CGCATGACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCG
                                                                   AAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAAC
                                                                                                                                       AGAACAGTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGCGCCCCAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="IMAGE:3611007"
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BE616613.1 GI:9898212
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Homo sapiens
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AUTHORS
TITLE
JOURNAL
COMMENT
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BG763582 958 bp mRNA linear EST 15-MAY-2001 602735987F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4861268 5', mRNA sequence. BG763582 BG763582.1 GI:14074235 EST.

9 655 99 714 720 770 780

840

887 897

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BUYPOUZI6 974 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8945604 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6459629
5', mRNA sequence.
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/lab host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
fluc BcoRIX/KhoI sites using the following S, adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capbbs-rémail.nih.gov
Tissue Procurement: ATCS
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Righ quality sequence stop: 603.
High quality sequence stop: 603.
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CCCACCACCTGACGGTGATCTTGGGCAGACATACCGGGTGGTCCCTGGCGAGGAGGAGC
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/tissue_type="melanotic melanoma, high MDR (cell line)"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab host="DH10B (phage-resistant)"
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/clone_lib="NHH MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: Xho1; Site 2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/khoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >Slobb for average insert size
1.8kD. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life_Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLCM1719 row: n column: 21
High quality sequence stop: 810.
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1 (bases 1 to 958)
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelt Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (Dases 1 to 709) NH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (Unpublished

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov

Plate: LLCM752 row: d column: 17

High quality sequence start: 3

High quality sequence stop: 701.

Location/Qualifiers

/organism="Homo sapiens"

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Berkeley) using ZAP-cDNA synthesis kit (Stratagene) a
Superscript II RT (Life Technologies). Note: this is
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BE732704
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Homo sapiens
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

BE732704 LOCUS DEFINITION

RESULT 15

/ Outsigning in the control of the c 382 120 300 322 442 180 502 240 562 622 360 682 420 742 480 9 CTGCCGCCCACTGCTTCCAGGAGGTTTCCGCCCCACCACCACGGTGATCTTGGGCA GAACATACCGGGTGGTCCCTGGCGAGGAGCAGAAATTTGAAGTCGAAAAATACATTG CGGATTCGTCCCGCTGTGCCCAGGAGAGCGTGGTCCGCACTGTGTGCCTTCCCCCGG cercercerceacergescereagacastracascerescereastracscarcaaassas 121 GGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAGGACAAGGAAGAAA GAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTG TCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAAT CCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGGAGTACTGTGATGTGC CCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGC GGCTCTTCGCCGACATCGCCTCCCACCCTGGCAGGCTGCCATCTTTGCCAAGCACAGGA GGTCGCCCGGAGAGCGGTTCCTGTGCGGGGCATACTCATCAGCTCCTGCTGGATTCTCT Gerceccesasascestrecrereresessesaracrearesereseresearrerer CTGCCGCCCACTGCTTCCAGGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCA TCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCTGCAGAAT CGGATTCGTCCCGCTGTGCCCAGGAGCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGG 1, 61.5%; Score 693.4; DB 10; Length 709; llarity 99.7%; Pred. No. 8.9e-170; Conservative 0; Mismatches 1; Indels 1; 421

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